

FIGURE 1Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds.
 ACCESSION M55983
 VERSION M55983.1 GI:181623
 KEYWORDS DNase I.
 SOURCE Human pancreus, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas"
 sig peptide 160..225
 /gene="DNase I"
 CDS 160..1008
 /gene="DNase I"
 /codon_start=1
 /product="DNase I"
 /protein_id="AAA63170.1"
 /db_xref="GI:181624"
 /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
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 LFVYRPDQVSAVDSYYDDGCEPCGNDFNREPAIVRFFSRFTEVREFAIVPLHAAPG
 DAVAEIDALYDVYLDVQEKGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
 PDSADTTATPTHCAYDRIIVVAGMLLRGAVVPDSALPFNFQAAAGLSDQLAQAI SDHYP
 VEVMLK"
 gene 160..1008
 /gene="DNase I"
 mat peptide 226..1005
 /gene="DNase I"
 /product="DNase I"
 BASE COUNT 226 a 305 c 282 g 226 t
 ORIGIN
 1 tcctgcacag gcagtgcctt gaagtgcctc ttcagagacc tttcttcata gactacttt
 61 ttttcttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
 121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
 181 gggcgctgc tggcactggc ggcctactg cagggggccg tgtccctgaa gatcgagcc
 241 ttcaacatcc agacattgg ggagaccaag atgtccatg ccaccctcgat cagctacatt
 301 gtgcagatcc tgagccgcta tgacatcgcc ctggccagg aggtcagaga cagccaccc
 361 actgccgtgg ggaagctgct ggacaaccc tc aatcaggatg caccagacac ctatcactac
 421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
 481 cctgaccagg tgtctcggt ggacagctac tactacatg atggctgcga gccctgcggg
 541 aacgacacct tcaaccgaga gccagccatt gtcaggtct tctcccggtt cacagaggcc
 601 agggagttt ccattgttcc cctgcatgcg gccccgggg acgcagtagc cgagatcgac
 661 gctctctatg acgtctaccc ggtatgtccaa gagaaatggg gcttggagga cgtcatgtt
 721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggc atccatccgc
 781 ctgtggacaa gccccaccc tt ccagtggctg atccccgaca gcgctgacac cacagctaca
 841 cccacgcact gtgcctatga caggatcgatg gttgcaggaa tgctgctccg aggcggcgtt
 901 gttcccgact cggctttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
 961 gccccagcca tcagtgcacca ctatccagtg gaggtgatgc tgaagtgc acgcctccc
 1021 cacaccaggta gaaactgcag

//

FIGURE 2

human DNase I construct

(A)

LOCUS MHDNASE.DN 783 bp mRNA **PRI** 06-MAR-1995
DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
ACCESSION M55963
NID q181623
KEYWORDS DNase I.
SOURCE Human pancreas, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Shak, S., Capon, D.J., Hellmies, R., Marsters, S.A. and Baker, C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
FEATURES Location/Qualifiers
source 1. .1039
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hDNase-18-1"
/tissue_type="pancreas"
sig_peptide 160. .225
/gene="DNase I"
CDS 160. .1008
/gene="DNase I"
/codon_start=1
/product="DNase I"
/db_xref="PID:q181624"
/translation="LKIAAFNIQTGETKMSNATLVSYIVQILSRYDIALVQEVRDSH
LTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYDDGCE
PCCNOTIFNREPAIVRFFSRFTEVREFAIPLHAAAPGDAVAEIDALYDVLQEKWGL
EDVIMLMGDFNAGCSYVVKPSQNSIIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
MLLRGAVVFDLAIFFNFQAYGLSDQIAQAIISDHYPVEVMT.K"
gene 160. .1008
/gene="DNase I"
mat_peptide 226. .1005
/gene="DNase I"
/product="DNase I"
BASE COUNT 168 a 236 c 220 g 159 t
ORIGIN
1 CTGAAGATCG CAGCCTTCAA CATCCAGACCA TTTGGGGAGA CCAAGATGTC CAATGCCACC
61 CTCGTAGCT ACATTTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
121 AGAGACAGCC ACCTGACTGC CGTGGGGAGA CTGCTGGACA ACCTCAATCA GGACGCACCA
181 GACACCTATC ACTACGTGGT CACTCACCCA CTGGGACCGGA ACAGCTATAA GGAGCGCTAC
241 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
301 TCGGAGCCCT GCGGGAAACGA CACCTTCARCA CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
361 CCGTTCACAG AGGTCAAGGGA GTTGGCCATT GTTCCCCTGC ATGCCGGCCCC GGGGGACGCA
421 GTAGGCCAGA TCGACGGCTCI CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
481 GAGGACGTCA TGTGATGGG CGACTTCAAT GCGGGCTGCA CCTATGTGAG ACCCTCCCAG
541 TGGTCATCCA TCCGCCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
601 GACACCCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
661 CTCGGAGGGG CCGTTGTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
721 CTGAGTGACC AACCTGGCCA AGGCACTAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
781 TGA

11

FIGURE 2(B)

LOCUS PAS155_GB. 858 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..75
 /note="160 to 225 of Untitled1"
 frag <10..>75
 /note="1 to 1039 of M55983.DNA [Split]"
 source <10..>75
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas [Split]"
 sig_peptide 10..75
 /gene="DNase I"
 CDS 10..>75
 /gene="DNase I"
 /codon_start="1"
 /product="DNase I"
 /db_xref="PID:g181624"
 /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
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 LFVYRPDQVSAVDSYYYDDGCEPCGNDFNREPAIVRFFSRFTEVREFAIVPLHAAPG
 D... [Split]"
 gene 10..>75
 /gene="DNase I [Split]"
 frag 76..858
 /note="1 to 783 of mod humanDNaseI"
 frag 76..858
 /note="1 to 72 of 104linker"
 frag join(76..>129,<131..147)
 /note="1 to 72 of 103linker [Split]"
 frag join(76..>126,<127..>129,<131..147)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGCGCTGC TGGCACTGGC GGCCCTACTG
 61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTGG GGAGACCAAG
 121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
 181 CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
 241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
 301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
 361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
 421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTG CCATTGTTCC CCTGCATGCG
 481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
 541 GAGAAATGGG GCTTGGAGGA CGTCATGTT ATGGCGACT TCAATGCGGG CTGCAGCTAT
 601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
 661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCAGT GTGCCTATGA CAGGATCGTG
 721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTAACTTC
 781 CAGGCTGCCT ATGGCCTGAG TGACCAAATG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
 841 GAGGTGATGC TGAAGTGA

FIGURE 3

(A) pAS6 - light chain

LOCUS HMFG1LC2.0 721 bp DNA
DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (BASES 1 TO 342)
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT SCANNED IN FROM JOURNAL
FEATURES
SITES

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeven paper)

BASE COUNT 197 a 202 c 182 g 140 t
ORIGIN ? LEADER SEQ

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACCTCGAC
61 ATCCAGATGA CCCAGAGCCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTGGCCTGG
181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTAA CCGACTTCAC CTTCACCATC
301 ACCACCCCTCC AGCCAGACGA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
421 TTCACTCTCC CGCCATCTGA TGAGCACTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCCTG
481 CTGAATAACT TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA
541 TCGGGTAACT CCCAGGAGAG TGTACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAC ACAAAAGTCTA CGCCTGCGAA
661 GTCACCCATC AGGGCCTGAG CTCGCCCCGTC ACAAAAGAGCT TCAACAGGGG AGAGTGTAG
721 A

11

Figure 3(B)

LOCUS HHMFG1KLC_ 730 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..730
 /note="1 to 721 of hHMFG1light chain"
 frag 10..730
 /note="1 to 72 of 104linker"
 frag join(10..>63,<65..81)
 /note="1 to 72 of 103linker [Split]"
 frag join(10..>60,<61..>63,<65..81)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTGTC
 61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
 121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
 181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
 241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTG AGCGGTAGCG GTAGCGGTAC CGACTTCACC
 301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
 361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 601 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
 721 GAGTGTAGA

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Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCHIELLVATATGVHSDIQMTQSPSSLSASVGDRVITCKSSQL
LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT
DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC

FIGURE 3

(D) pAS6 - heavy chain

LOCUS HMF1HC.D 1404 bp DNA
 DEFINITION HUMANISED HMFG1 heavy chain
 ACCESSION HMF1H
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT VH domain SCANNED IN FROM JOURNAL
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 333 a 439 c 379 g 253 t
 ORIGIN ?
 LERPER -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCOCAG
 61 GTGCAAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAGCTTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAGAGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAARGGGCC TCGAGTGGGT CGGAGAQATT TTACCTGGAA GTAATAATTC TAGATAACAAT
 241 GAGAAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCTTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACATCA
 541 GGCGCCCTGA CCAGGGGGT GCACACCTTC CCGGCTGTCC TACAGTCTTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAGGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC XACAGGCCAG ACCGTGCCA GCACCTGAA TCCTGGGGG ACCGTCAAGTC
 781 TTCCCTCTTCC CCCCAAAACC CAAGGACACC CTCAATGATCT CCCGGACCCC TGAGGTCA
 841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCCGGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCTCTCAC CGTCTCGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAA
 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG
 1141 AACCAAGTCA GCCTGACCTG CCTGGTCAA GGCTCTATC CCAGCGACAT CGCCGTGGAG
 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAC TACAAGACCA CGCTCTCCGT GCTGGACTCC
 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC CGAGAAGAGC
 1381 CTCTCCCTGT CTCCGGTAA ATGA

► Antibody Driven Fusions made here (eg pAS 34-39.)

End of lower hinge region of heavy chain. PAPE amino
Add SEQ. Fab' fusions were made at this point.

Those with HYBRID HINGES ARE ALTERED FURTHER
UP

ie.

► this part GACAAAATCACA
is → D k t H T

AFTER THIS SEQUENCE YOU GET THE

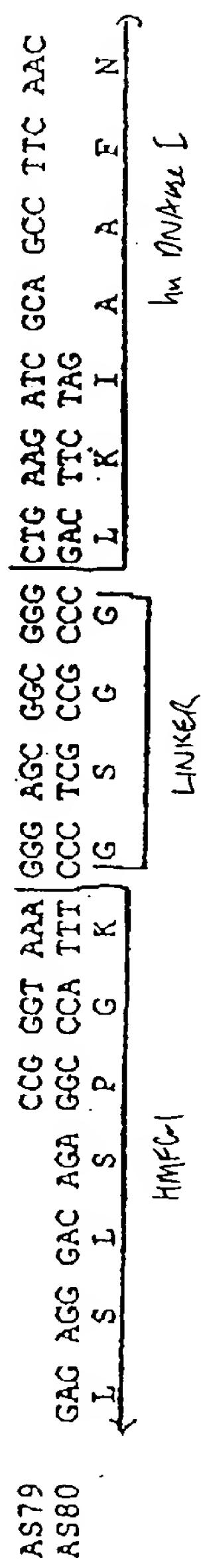
HYBRID HINGE + LINKER SEQUENCES

Then DrAze I (eg Fab-ONbase construct pAS302)

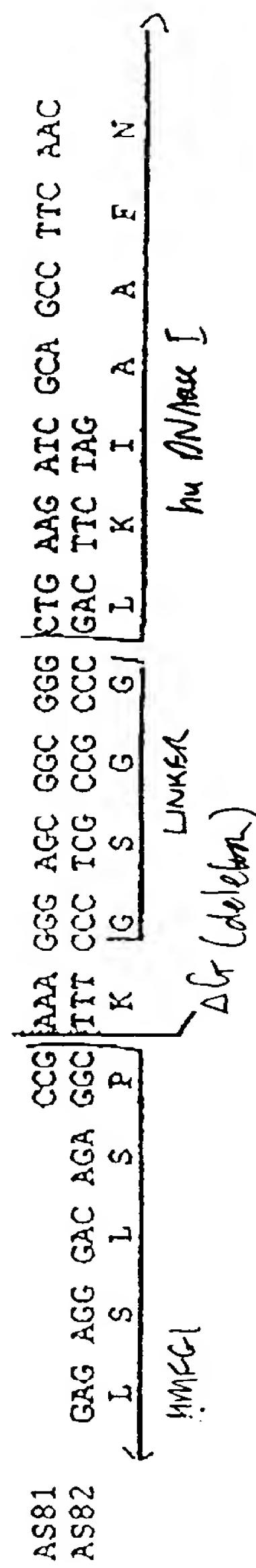
(A.)

Oligos involved in the fusion of whole antibody-DNase

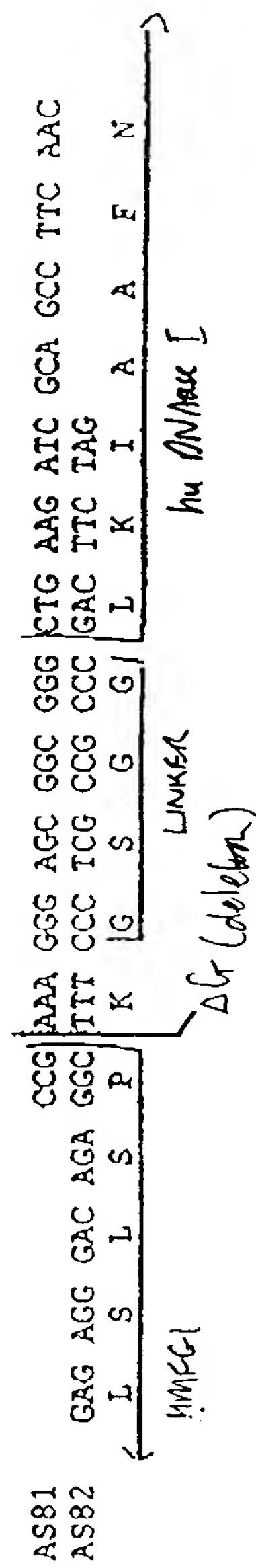
Constructs pAS34/37



Constructs pAS35/38



Constructs pAS36/39



Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

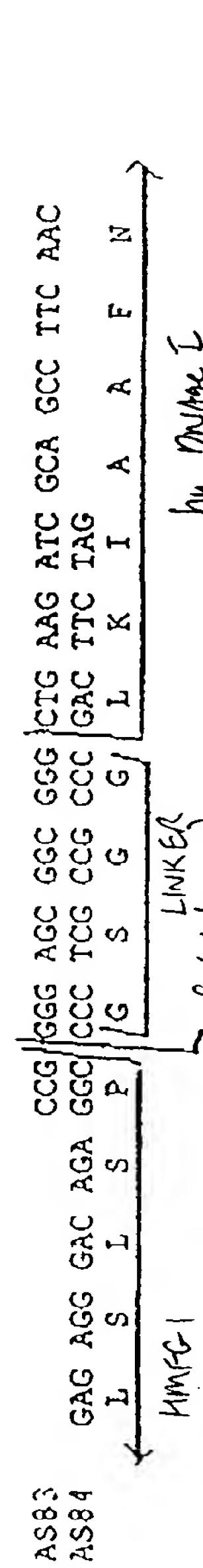


FIGURE 9

(B)

Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs PAS101/105

AS86 GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC
 AS87 GGT GGC ACG GGT CTT GGA CTT CCG CCC GAC TTC TAG
 ← P C P A P E G G G
 ← HMFG1 (hinge)

h_u DNase I

SHORT
LINKER

Constructs PAS102/106

AS88 CTC TTT TGA TGT TGT ACG ACA CAG CTC ACA GGT GGC GCA GAG GGG AGC GGC GGG CTC AAG ATC GCA GCC TTC
 AS89 CTC TTT TGA TGT TGT ACG ACA CAG CTC ACA GGT GGC GCA GAG GGG AGC GGC GGG CTC AAG ATC GCA GCC TTC
 ← D X T H T C C V E C P P C P E G S G G
 ← HMFG1

HYBRID HINGE

LONG LINKER

Constructs PAS103/107

AS90 GTC GAG TGT CCA CCG TGT CCA GCA GAG GGC GGG CTC AAG ATC GCA GCC TTC
 AS91 GTC GAG TGT CCA CCG TGT CCA GCA GAG GGC GGG CTC AAG ATC GCA GCC TTC
 ← D X T H T C C V E C P P C P E G G G
 ← HMFG1

HYBRID HINGE

SHORT
LINKER

FIGURE 4

FIGURE 5

(A) pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 434 g 308 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTCTAGATAACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTCA GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAG GGAGCGGCCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCAGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTACACA
1141 GAGGTCAAGGG AGTTTGCCAT TGTTCCCTG CATGCGGCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCAGGTGGAC AGCTATGTGA GACCCCTCCA GTGGTCATCC
1321 ATCCGCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

Figure 5(B)

LOCUS FDDNASE23_ 1554 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<787..1554)
 /note="1 to 1554 of 23.dna [Split]"
 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
 /note="1 to 78 of 1021linker [Split]"
 BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
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Figure S(c)

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 ACCESSION -
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 SOURCE -
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 frag join(730..>744,<745..795)
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
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 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGÄ CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
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 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
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 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
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 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
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File : PAS23.DNA
 Range : 1 - 1554 Mode : Normal
 Codon Table : Universal

FIGURE S(D)

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S Q V Q L V Q S G A E V K K P G A S					
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GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
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D T A V Y Y C A R S Y D F A W F A Y					
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W G Q G T L V T V S S A S T K G P S					
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V F P L A P S S K S T S G G T A A L					
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G C L V K D Y F P E P V T V S W N S					
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V E P K S C D K T H T C P P C P A P

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W	G	L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y
1305		1314		1323		1332		1341		1350							
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D	R	I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S
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A	L	P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q
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GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'			
A	I	S	D	H	Y	P	V	E	V	M	L	K	*				

FIGURE 6

(A) pAS27

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 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
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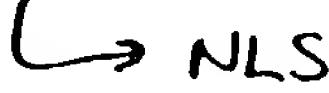

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Figure 6(c)

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 BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER
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 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT A CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
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 1081 TCGGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAAGGG A GTTGCCTATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
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File : PAS27.DNA
Range : 1 - 584 Mode : Normal
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Page 6 (D)

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S Q V Q L V Q S G A E V K K P G A S					
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G A L T S G V H T F P A V L Q S S G					

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L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
-----	-----	-----	-----	-----	-----
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
-----	-----	-----	-----	-----	-----
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
-----	-----	-----	-----	-----	-----
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
-----	-----	-----	-----	-----	-----
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG					
-----	-----	-----	-----	-----	-----
S E P L G R N S Y K E R Y L F V Y R					
1035	1044	1053	1062	1071	1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
-----	-----	-----	-----	-----	-----
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG					
-----	-----	-----	-----	-----	-----
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
-----	-----	-----	-----	-----	-----
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA
 A V A E D A L Y D V Y L V Q E K
 1251 1260 1269 1278 1287 1296
 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT
 W G L E D V M L M G D F N A G C S Y
 1305 1314 1323 1332 1341 1350
 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG
 V R P S Q W S S I R L W T S P T F Q
 1359 1368 1377 1386 1395 1404
 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT
 W L I P D S A D T T A T P T H C A Y
 1413 1422 1431 1440 1449 1458
 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG
 D R I V V A G M L L R G A V V P D S
 1467 1476 1485 1494 1503 1512
 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA
 A L P F N F Q A A Y G L S D Q L A Q
 1521 1530 1539 1548 1557 1566
 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA
 A I S D H Y P V E V M L K G G G P K
 1575 1584
 AAG AAG CGC AAG GTT TGA 3'
K K R K V *

FIGURE 7

(A) pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34
DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file)
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS79 and AS80
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 501 a 677 c 607 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAAGAGC
1381 CTCTCCCTGT CTCCGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAAGGTG
1681 TCTCGGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCAGGTTCA CAGAGGTAG CAGAGGTAG GGAGTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCAGGGCT GCAGCTATGT GAGACCCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

//

File : PAS34.DNA
 Range : 1 - 2196 Mode : Normal
 Codon Table : Universal

FIGURE 7(B)

	9	18	27	36	45	54
5.	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					
	603	612	621	630	639	648
	CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TGT GGC ACC CAG					
	L Y S L S S V V T V P S S S L G T Q					
	657	666	675	684	693	702

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C V N H K P S N T K V D K K

711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P

765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T

819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H

873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N

927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S

981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K

1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K

1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L

1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D

1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T

1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V

1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC	TAC ACG CAG AAG AGC CTC TCC CTG T	G GGT AAA GGG			
A L H N H Y T Q K S L S L S P G K <u>G</u>					
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
<u>S</u> <u>G</u> <u>G</u> L K I A A F N I Q T F G E T K					
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
L D N L N Q D A P D T Y H Y V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
Q V S A V D S Y Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
I P D S A D T T A T P T H C A Y D R					

2061	070	2079	2088	7	2106												
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	SAC	TCG	GCT	CTT
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
2115	2124	2133	2142	2151	2160												
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
2169	2178	2187	2196														
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
S	D	H	Y	P	V	E	V	M	L	K	*						

(A) pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS81 and AS82
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
 SITES Note
 BASE COUNT 500 a 677 c 606 g 410 t
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTTTCC CCCAAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGGC
1381 CTCTCCCTGT CTCCGAAGG GAGCGGGCGGG CTGAAGATCG CAGCCTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGGAAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAAGGA GTTGCCATT
1801 GTTCCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA
  
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//

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					
	603	612	621	630	639	648
	CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
	L Y S L S S V V T V P S S S L G T Q					
	657	666	675	684	693	702

ACC TAC ATC TGC C G TG AAT CAC AAG CCC AGC AAC ACC A G TG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K

711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P

765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T

819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H

873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N

927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S

981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K

1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K

1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L

1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D

1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T

1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V

1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC	TAC ACG CAG AAG AGC CTC TCC CTG TO	G AAG GGG AGC			
A L H N H Y T Q K S L S L S P K G S					
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
<u>G</u> <u>G</u> L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
V S A V D S Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG					
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC					
P D S A D T T A T P T H C A Y D R I					

2061 2070 2079 2088 2097 2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC
V V A G M L L R G A V V P D S A L P
2115 2124 2133 2142 2151 2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT
F N F Q A A Y G L S D Q L A Q A I S
2169 2178 2187
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
D H Y P V E V M L K *

(A) pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36
 DEFINITION Clone 18.24.1 with residue 1392 T > C
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS83 and AS84
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES Residue 1392 T > C silent S to S mutation
 SITES Note
 BASE COUNT 498 a 678 c 605 g 409 t
 ORIGIN ?

```

 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCAGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCCTGGCTG AAGATCGCAG CCTTCAACAT CCAGACATT
1441 GGGGAGACCA AGATGTCAA TGCCACCCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTATGT TGATGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGAACAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA
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File : PAS36.DNA
 Range : 1 - 2190 Mode : Normal
 Codon Table : Universal

FIGURE 9 (B)

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					
603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

1359	1368	1377	1386	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC				
A L H N H Y T Q K S L S L S P G S G				
1413	1422	1431	1440	1449
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC				
G L K I A A F N I Q T F G E T K M S				
1467	1476	1485	1494	1503
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC				
N A T L V S Y I V Q I L S R Y D I A				
1521	1530	1539	1548	1557
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC				
L V Q E V R D S H L T A V G K L L D				
1575	1584	1593	1602	1611
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG				
N L N Q D A P D T Y H Y V V S E P L				
1629	1638	1647	1656	1665
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG				
G R N S Y K E R Y L F V Y R P D Q V				
1683	1692	1701	1710	1719
TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC				
S A V D S Y Y D D G C E P C G N D				
1737	1746	1755	1764	1773
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC				
T F N R E P A I V R F F S R F T E V				
1791	1800	1809	1818	1827
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG				
R E F A I V P L H A A P G D A V A E				
1845	1854	1863	1872	1881
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG				
I D A L Y D V Y L D V Q E K W G L E				
1899	1908	1917	1926	1935
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC				
D V M L M G D F N A G C S Y V R P S				
1953	1962	1971	1980	1989
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC				
Q W S S I R L W T S P T F Q W L I P				
2007	2016	2025	2034	2043
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG				
D S A D T T A T P T H C A Y D R I V				

2061 2070 2079 2088 2097 2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT
V A G M L L R G A V V P D S A L P F
2115 2124 2133 2142 2151 2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC
N F Q A A Y G L S D Q L A Q A I S D
2169 2178 2187
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
H Y P V E V M L K *

(A) pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37
 DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) plus NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 511 a 683 c 619 g 413 t
 ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACCTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCCT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
 841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCCTGGAG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
 1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGATGA GCTGACCAAG
 1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
 1381 CTCTCCCTGT CTCCGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAAGGTG
 1681 TCTGCCTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGGGGAA CGACACCTTC
 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCCTGTTCA CAGAGGTAG GGAGTTGCC
 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
 1921 AATGCGGGCT GCAGCTATGT GAGACCCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
 1981 CCCACCTTCC AGTGGCTGAT CCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
 2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCTGAGTG ACCAACTGGC CCAAGCCATC
 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGCG GACCAAAAAA GAAGCGCAAG
 2221 GTTTGA

//

NLS

File : PAS37.DNA
 Range : 1 - 2226 Mode : Normal
 Codon Table : Universal

FIGURE 10 (B)

	9	18	27	36	45	54												
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	63		72			81			90			99			108			
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	117		126			135			144			153			162			
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	171		180			189			198			207			216			
	TGG	GTG	CGC	CAG	GCT	CCA	GGG	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225		234			243			252			261			270			
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279		288			297			306			315			324			
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	333		342			351			360			369			378			
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	387		396			405			414			423			432			
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441		450			459			468			477			486			
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	495		504			513			522			531			540			
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549		558			567			576			585			594			
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G
	603		612			621			630			639			648			
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
	657		666			675			684			693			702			

ACC	TAC	ATC	TGC	AC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AA	GTG	GAC	AAG	AAA
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711				720			729			738			747			756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765				774			783			792			801			810	
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T
819				828			837			846			855			864	
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H
873				882			891			900			909			918	
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N
927				936			945			954			963			972	
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S
981				990			999			1008			1017			1026	
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K
1035				1044			1053			1062			1071			1080	
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
1089				1098			1107			1116			1125			1134	
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L
1143				1152			1161			1170			1179			1188	
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D
1197				1206			1215			1224			1233			1242	
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T
1251				1260			1269			1278			1287			1296	
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V
1305				1314			1323			1332			1341			1350	
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E

1359 1368 1377 1386 1404
 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG
 A L H N H Y T Q K S L S L S P G K G
 1413 1422 1431 1440 1449 1458
 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
 S G G L K I A A F N I Q T F G E T K
 1467 1476 1485 1494 1503 1512
 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
 M S N A T L V S Y I V Q I L S R Y D
 1521 1530 1539 1548 1557 1566
 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
 I A L V Q E V R D S H L T A V G K L
 1575 1584 1593 1602 1611 1620
 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
 L D N L N Q D A P D T Y H Y V V S E
 1629 1638 1647 1656 1665 1674
 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
 P L G R N S Y K E R Y L F V Y R P D
 1683 1692 1701 1710 1719 1728
 CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
 Q V S A V D S Y Y Y D D G C E P C G
 1737 1746 1755 1764 1773 1782
 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA
 N D T F N R E P A I V R F F S R F T
 1791 1800 1809 1818 1827 1836
 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
 E V R E F A I V P L H A A P G D A V
 1845 1854 1863 1872 1881 1890
 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
 A E I D A L Y D V Y L D V Q E K W G
 1899 1908 1917 1926 1935 1944
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
 L E D V M L M G D F N A G C S Y V R
 1953 1962 1971 1980 1989 1998
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
 P S Q W S S I R L W T S P T F Q W L
 2007 2016 2025 2034 2043 2052
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
 I P D S A D T T A T P T H C A Y D R

2061 2070 2079 2088 2097 2106
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
 I V V A G M L L R G A V V P D S A L
 2115 2124 2133 2142 2151 2160
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
 P F N F Q A A Y G L S D Q L A Q A I
 2169 2178 2187 2196 2205 2214
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG
 S D H Y P V E V M L K G G G P K K K
 2223
 CGC AAG GTT TGA 3'
R K V *

(A) pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G) +NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS81 and AS82
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
 SITES Note
 BASE COUNT 510 a 683 c 618 g 412 t
 ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAACCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCCT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACACA
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
 1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGGC
 1381 CTCTCCCTGT CTCCGAAGG GAGCGGGGG CTGAAGATCG CAGCCTCAA CATCCAGACA
 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAAGCT ACATTGTGCA GATCCTGAGC
 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGGAAAG
 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGT ACAGGCCTGA CCAGGTGTCT
 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
 1741 CGAGAGCCAG CCATTGTCAAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTGTCCATT
 1801 GTTCCCCCTGC ATGCGGCCCG GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACGTGCCC
 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTCC CGACTCGGCT
 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACCA AACTGGCCCA AGCCATCAGT
 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGCGGAC CCAAAAAGAA GCGCAAGGTT
 2221 TGA

L NLS

//

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					
	603	612	621	630	639	648
	CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
	L Y S L S V V T V P S S S L G T Q					
	657	666	675	684	693	702

ACC TAC ATC TGC GTG AAT CAC AAG CCC AGC AAC ACC A TG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

1359 1368 1377 1386 395 1404
 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC
 A L H N H Y T Q K S L S L S P K G S
 1413 1422 1431 1440 1449 1458
 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG
G G L K I A A F N I Q T F G E T K M
 1467 1476 1485 1494 1503 1512
 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC
 S N A T L V S Y I V Q I L S R Y D I
 1521 1530 1539 1548 1557 1566
 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG
 A L V Q E V R D S H L T A V G K L L
 1575 1584 1593 1602 1611 1620
 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA
 D N L N Q D A P D T Y H Y V V S E P
 1629 1638 1647 1656 1665 1674
 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG
 L G R N S Y K E R Y L F V Y R P D Q
 1683 1692 1701 1710 1719 1728
 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC
 V S A V D S Y Y D D G C E P C G N
 1737 1746 1755 1764 1773 1782
 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG
 D T F N R E P A I V R F F S R F T E
 1791 1800 1809 1818 1827 1836
 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC
 V R E F A I V P L H A A P G D A V A
 1845 1854 1863 1872 1881 1890
 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG
 E I D A L Y D V Y L D V Q E K W G L
 1899 1908 1917 1926 1935 1944
 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC
 E D V M L M G D F N A G C S Y V R P
 1953 1962 1971 1980 1989 1998
 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC
 S Q W S S I R L W T S P T F Q W L I
 2007 2016 2025 2034 2043 2052
 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC
 P D S A D T T A T P T H C A Y D R I

2061 2070 2079 2088 2097 2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC
V V A G M L L R G A V V P D S A L P
2115 2124 2133 2142 2151 2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT
F N F Q A A Y G L S D Q L A Q A I S
2169 2178 2187 2196 2205 2214
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC
D H Y P V E V M L K G G G P K K K R
2223
AAG GTT TGA 3'
K V *

FIGURE

(A) pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39
 DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS83 and AS84
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES Residue 1392 T > C silent S to S mutation
 SITES Note
 BASE COUNT 508 a 684 c 617 g 411 t
 ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCAC AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
 781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACACA
 841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
 1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG
 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCGT GCTGGACTCC
 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGAC
 1381 CTCTCCCTGT CccCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATT
 1441 GGGGAGACCA AGATGTCCAA TGCCACCCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
 1501 TACGACATCG CCCTGGTCCA GGAGGTCAAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
 1561 CTGGACAACC TCAATCAGGA CGCACCAAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
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 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGCACCAAC TGGCCCAAGC CATCAGTGAC
 2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCAGGACCCA AAAAGAAGCG CAAGGTTTGA

//

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC					
M	G	W	S	C	I
I	I	L	F	L	V
A	T	A	T	G	V
					H

63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S	Q	V	Q	L	V
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V	K	V	S	C	K
A	S	G	Y	T	F
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W	V	R	Q	A	P
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G	S	N	N	S	R
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R	D	T	S	T	N
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D	T	A	V	Y	Y
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W	G	Q	G	T	L
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V	F	P	L	A	P
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G	C	L	V	K	D
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G	A	L	T	S	G
603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L	Y	S	L	S	S
657	666	675	684	693	702

ACC	TAC	ATC	TG	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	A	TG	GAC	AAG	AAA	
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711		720		729		738		747		756							
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765		774		783		792		801		810							
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T
819		828		837		846		855		864							
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H
873		882		891		900		909		918							
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N
927		936		945		954		963		972							
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S
981		990		999		1008		1017		1026							
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K
1035		1044		1053		1062		1071		1080							
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
1089		1098		1107		1116		1125		1134							
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L
1143		1152		1161		1170		1179		1188							
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D
1197		1206		1215		1224		1233		1242							
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T
1251		1260		1269		1278		1287		1296							
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V
1305		1314		1323		1332		1341		1350							
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E

1359 68 1377 1386 1404
 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC G GGG AGC GGC
 A L H N H Y T Q K S L S L S P G S G
 1413 1422 1431 1440 1449 1458
 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC
 G L K I A A F N I Q T F G E T K M S
 1467 1476 1485 1494 1503 1512
 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC
 N A T L V S Y I V Q I L S R Y D I A
 1521 1530 1539 1548 1557 1566
 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC
 L V Q E V R D S H L T A V G K L L D
 1575 1584 1593 1602 1611 1620
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 N L N Q D A P D T Y H Y V V S E P L
 1629 1638 1647 1656 1665 1674
 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG
 G R N S Y K E R Y L F V Y R P D Q V
 1683 1692 1701 1710 1719 1728
 TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC
 S A V D S Y Y Y D D G C E P C G N D
 1737 1746 1755 1764 1773 1782
 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC
 T F N R E P A I V R F F S R F T E V
 1791 1800 1809 1818 1827 1836
 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG
 R E F A I V P L H A A P G D A V A E
 1845 1854 1863 1872 1881 1890
 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG
 I D A L Y D V Y L D V Q E K W G L E
 1899 1908 1917 1926 1935 1944
 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC
 D V M L M G D F N A G C S Y V R P S
 1953 1962 1971 1980 1989 1998
 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC
 Q W S S I R L W T S P T F Q W L I P
 2007 2016 2025 2034 2043 2052
 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG
 D S A D T T A T P T H C A Y D R I V

2061 2070 2079 2088 2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT
V A G M L L R G A V V P D S A L P F
2115 2124 2133 2142 2151 2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC
N F Q A A Y G L S D Q L A Q A I S D
2169 2178 2187 2196 2205 2214
CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG
H Y P V E V M L K G G G P K K K R K

GTT TGA 3'

V *

FIGURE 13

(A) pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 343 a 467 c 430 g 308 t
 ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTGCAGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACAGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCAGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAAATG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Figure 13 (B)

LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1548)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAAGGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTGAG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTCGGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCCT TGCCTATGA CAGGATCGTG GTTGCAGGGG TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Figure 13c

LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000
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 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<790..1557)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER
 ORIGIN -
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT A CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GTTCAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTT
 1021 GTGTACAGGC CTGACCAGGT GTCTCGGGT GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGGTTC
 1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCCGGGGGA CGCAGTAGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAAGCTATG TGAGACCCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCAAC TATCCAGTGG AGGTGATGCT GAAGTGA

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File : PAS101.DNA
Range : 1 - 548 Mode : Normal
Codon Table : Universal

PICTURE B (D)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
9 18 27 36 45 54
M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
G A L T S G V H T F P A V L Q S S G

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
-----	-----	-----	-----	-----	-----
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
-----	-----	-----	-----	-----	-----
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
-----	-----	-----	-----	-----	-----
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
-----	-----	-----	-----	-----	-----
E G G L K I A A F N I Q T F G E T K					
819	828	837	846	855	864
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
-----	-----	-----	-----	-----	-----
M S N A T L V S Y I V Q I L S R Y D					
873	882	891	900	909	918
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
-----	-----	-----	-----	-----	-----
I A L V Q E V R D S H L T A V G K L					
927	936	945	954	963	972
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
-----	-----	-----	-----	-----	-----
L D N L N Q D A P D T Y H Y V V S E					
981	990	999	1008	1017	1026
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
-----	-----	-----	-----	-----	-----
P L G R N S Y K E R Y L F V Y R P D					
1035	1044	1053	1062	1071	1080
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
-----	-----	-----	-----	-----	-----
Q V S A V D S Y Y Y D D G C E P C G					
1089	1098	1107	1116	1125	1134
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
-----	-----	-----	-----	-----	-----
N D T F N R E P A I V R F F S R F T					
1143	1152	1161	1170	1179	1188
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
-----	-----	-----	-----	-----	-----
E V R E F A I V P L H A A P G D A V					
1197	1206	1215	1224	1233	1242

GCC	GAG	ATC	GAC	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	GAG	AAA	TGG	GGC		
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G
1251	1260	1269	1278	1287	1296												
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R
1305	1314	1323	1332	1341	1350												
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L
1359	1368	1377	1386	1395	1404												
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R
1413	1422	1431	1440	1449	1458												
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
1467	1476	1485	1494	1503	1512												
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
1521	1530	1539	1548														
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
S	D	H	Y	P	V	E	V	M	L	K	*						

FIGURE

(A) pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna) (see Figure 2)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 345 a 469 c 440 g 312 t
 ORIGIN

```

 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACCTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA
  //
```

Figure 14 (B)

CUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CC GGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATTTGT
 721 GACAAAACTC ACACATGCTG TGTGAGTGT CCACCGTGTG CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCA GTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCA GTGAG TCTGCCTGG ACAGCTACTA CTACGATGAT
 1081 GGCTCGGAGC CCTGCAGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCAGGTTCA CAGAGGTCA GGAGTTGCC ATTGTTCCCC TGCA TGCGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCAGTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTCCCT TTAACCTCCA GGCTGCCTAT
 1501 GGCGTGAATC ACCAACTGGC CCAAGCCATC AGTGGACCACT ATCCAGTGGG GGTGATGCTG
 1561 AAGTGA

Figure 14 (c)

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
frag 10..1575
/note="1 to 1566 of FdDNase102correct"
BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER
ORIGIN -
1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAAG GACTACTTCC CCGAACCGGT GACGGTGTG
541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGCTGTCC ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGT CACCGTGTCC AGCACCAGAG
781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATGCCCTG
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
1021 AAGGAGCGCT ACCTGTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAAG GAGTTGCCA TTGTTCCCCT GCATGCGGCC
1201 CGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCAGTTCA ATGCGGGCTG CAGCTATGTG
1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
1441 GCAGGGATGC TGCTCCGAGG GGCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
1561 GTGATGCTGA AGTGA

File : PAS102.DNA
 Range : 1 - 1566 Mode : Normal
 Codon Table : Universal

FIGURE 14 (D)

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
C A L T S G V H T F P A V L Q S S G					

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657			666			675			684			693			702		
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711			720			729			738			747			756		
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
765			774			783			792			801			810		
TGC	CCA	GCA	CCT	GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
C	P	A	P	E	G	S	G	G	L	K	I	A	A	F	N	I	Q
819			828			837			846			855			864		
ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	F	G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q
873			882			891			900			909			918		
ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
I	L	S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L
927			936			945			954			963			972		
ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	A	V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y
981			990			999			1008			1017			1026		
CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	Y	V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L
1035			1044			1053			1062			1071			1080		
TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	V	Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D
1089			1098			1107			1116			1125			1134		
GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	C	E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R
1143			1152			1161			1170			1179			1188		
TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	F	S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A
1197			1206			1215			1224			1233			1242		

GCC CCG GGG GAC A GTA GCC GAG ATC GAC GCT CTC TAT GTC TAC CTG GAT
 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
 Q L A Q A I S D H Y P V E V M L K *

FIGURE 15

(A) pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 344 a 468 c 436 g 312 t
 ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCAC
 61 CTCCAG
 121 TGCAAGGCTT CTGGCTACAC CTTCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTAC
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGC
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCG
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCAC
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGT
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGG
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTAC
 661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGG
 781 GGGGCTGAGACAG CCTTCAACAT CCAGACATTG AGATGTCCAA TGCCACCC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGG
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCG
 1021 TTCGTGTACA GGCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGG
 1081 GGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCT
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGAC
 1201 GGCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGG
 1261 GACGTCAATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCC
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCG
 1381 ACACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATG
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGG
 1501 AGTGAACAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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Figure 1S (B)

LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000
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 ORGANISM -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
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 BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCACT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTGAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAAGGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTCCCGA CTCGGCTCTT CCCTTTAATC TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

Figure 1S (c)

LOCUS	FDDNASE103	1569	BP	SS-DNA	SYN	29-AUG-2000					
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ACCESSION	-										
KEYWORDS	-										
SOURCE	-										
FEATURES	Location/Qualifiers										
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	/note="1 to 1560 of PAS103.dna [Split]"										
frag	730..801										
	/note="1 to 72 of 103/107linker"										
frag	join(730..>780,<781..801)										
	/note="1 to 78 of 102linker [Split]"										
BASE COUNT	345	A	473	C	438	G	313	T	0	OTHER	
ORIGIN	-										
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61	CACTCCCAGG	TGCAGCTGGT	GCAGTCTGGG	GCAGAGGTGA	AAAAGCCTGG	GGCCTCAGTG					
121	AAGGTGTCCT	GCAAGGGCTTC	TGGCTACACC	TTCAGTGCT	ACTGGATAGA	GTGGGTGCGC					
181	CAGGCTCCAG	GAAAGGGCCT	CGAGTGGGTC	GGAGAGATT	TACCTGGAAG	TAATAATTCT					
241	AGATACAATG	AGAAGTTCAA	GGGCCGAGTG	ACAGTCACTA	GAGACACATC	CACAAACACA					
301	GCCTACATGG	AGCTCAGCAG	CCTGAGGTCT	GAGGACACAG	CCGTCTATT	CTGTGCAAGA					
361	TCCTACGACT	TTGCCTGGTT	TGCTTACTGG	GGCCAAGGGA	CTCTGGTCAC	AGTCTCCTCA					
421	GCCTCCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCC	CCTCCAAGAG	CACCTCTGGG					
481	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTG					
541	TGGAACTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA					
601	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC					
661	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGTTGAGCCC					
721	AAATCTTGTG	ACAAAACCTCA	CACATGCTGT	GTCGAGTGTC	CACCGTGTCC	AGCACCAGAG					
781	GGCGGGCTGA	AGATCGCAGC	CTTCAACATC	CAGACATTG	GGGAGACCAA	GATGTCCAAT					
841	GCCACCCCTG	TCAGCTACAT	TGTGCAGATC	CTGAGCCGCT	ACGACATCGC	CCTGGTCCAG					
901	GAGGTCAAGAG	ACAGCCACCT	GACTGCCGTG	GGGAAGCTGC	TGGACAACCT	CAATCAGGAC					
961	GCACCAGACA	CCTATCACTA	CGTGGTCAGT	GAGCCACTGG	GACGGAACAG	CTATAAGGAG					
1021	CGCTACCTGT	TCGTGTACAG	GCCTGACCAG	GTGTCTGCGG	TGGACAGCTA	CTACTACGAT					
1081	GATGGCTGCG	AGCCCTGCGG	GAACGACACC	TTCAACCGAG	AGCCAGCCAT	TGTCAGGTT					
1141	TTCTCCCGGT	TCACAGAGGT	CAGGGAGTT	GCCATTGTT	CCCTGCATGC	GGCCCCGGGG					
1201	GACGCAGTAG	CCGAGATCGA	CGCTCTCTAT	GACGTCTACC	TGGATGTCCA	AGAGAAATGG					
1261	GGCTTGGAGG	ACGTCATGTT	GATGGGCGAC	TTCAATGCGG	GCTGCAGCTA	TGTGAGACCC					
1321	TCCCAGTGGT	CATCCATCCG	CCTGTGGACA	AGCCCCACCT	TCCAGTGGCT	GATCCCCGAC					
1381	AGCGCTGACA	CCACAGCTAC	ACCCACGCAC	TGTGCCTATG	ACAGGATCGT	GGTTGCAGGG					
1441	ATGCTGCTCC	GAGGGGCCGT	TGTTCCCGAC	TCGGCTCTTC	CCTTTAACTT	CCAGGCTGCC					
1501	TATGGCCTGA	GTGACCAACT	GGCCCAAGCC	ATCAGTGACC	ACTATCCAGT	GGAGGTGATG					
1561	CTGAAGTGA										

• File : PAS103.DNA
Range : 1 - 560 Mode : Normal
Codon Table : Universal

PIRURE IS (D)

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					

603 612 621 630 639 648
 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GCC ACC CAG
 L Y S L S S V V T V P S S S L G T Q

 657 666 675 684 693 702
 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K

 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
 V E P K S C D K T H T C C V E C P P

 765 774 783 792 801 810
 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT
 C P A P E G G L K I A A F N I Q T F

 819 828 837 846 855 864
 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG
 G E T K M S N A T L V S Y I V Q I L

 873 882 891 900 909 918
 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC
 S R Y D I A L V Q E V R D S H L T A

 927 936 945 954 963 972
 GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC
 V G K L L D N L N Q D A P D T Y H Y

 981 990 999 1008 1017 1026
 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG
 V V S E P L G R N S Y K E R Y L F V

 1035 1044 1053 1062 1071 1080
 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC
 Y R P D Q V S A V D S Y Y Y D D G C

 1089 1098 1107 1116 1125 1134
 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC
 E P C G N D T F N R E P A I V R F F

 1143 1152 1161 1170 1179 1188
 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG
 S R F T E V R E F A I V P L H A A P

 1197 1206 1215 1224 1233 1242

GGG GAC GCA GTA C GAG ATC GAC GCT CTC TAT GAC GTC CTG GAT GTC CAA
 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
 A Q A I S D H Y P V E V M L K *

FIGURE

(A) pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
 Position 924 G to A by ggg to gag
 Linker GR instead of GG (position 777)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 346 a 468 c 434 g 312 t
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACCTCCCAG
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121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
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841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTAGA
901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GCCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACCGAGTA
1201 GCCGAGATCG ACGCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCAATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAAGT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
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Figure 1b (b)

FOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
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 frag 721..792
 /note="1 to 72 of 104linker"
 frag join(721..>774,<776..792)
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 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
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 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTTCAGA
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 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTGGAG
 1261 GACGTCTGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
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File : PAS104.DN
Range : 1 1560 Mode : Normal
Codon Table : Universal

Figure 16 (C)

9	18	27	36	45	54
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M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

603 612 621 630 639 648
 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
 L Y S L S S V V T V P S S S L G T Q

 657 666 675 684 693 702
 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K

 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG
 V E P K S C D K T H T C C V E C P P

 765 774 783 792 801 810
 TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT
 C P A P E G R L K I A A F N I Q T F

 819 828 837 846 855 864
 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG
 G E T K M S N A T L V S Y I V Q I L

 873 882 891 900 909 918
 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC
 S R Y D I A L V Q E V R D S H L T A

 927 936 945 954 963 972
 GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC
 V E K L D N L N Q D A P D T Y H Y

 981 990 999 1008 1017 1026
 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG
 V V S E P L G R N S Y K E R Y L F V

 1035 1044 1053 1062 1071 1080
 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC
 Y R P D Q V S A V D S Y Y Y D D G C

 1089 1098 1107 1116 1125 1134
 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC
 E P C G N D T F N R E P A I V R F F

 1143 1152 1161 1170 1179 1188
 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG
 S R F T E V R E F A I V P L H A A P

 1197 1206 1215 1224 1233 1242

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
 A Q A I S D H Y P V E V M L K *

FIGURE 17

(A) pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS (pAS105)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 353 a 473 c 442 g 310 t
 ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCAC
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTGG GGAGACCAAG ATGTCCAATG CCACCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTCGGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGTTCT TCTCCCGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCCGG CTGCAGCTAT GTGAGACCCCT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGG CGGACCCAAA
 1561 AAGAAGCGCA AGGTTTGA

//

NLS

Figure 17(B)

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1578)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 353 A 471 C 443 G 311, T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATTTGT
 721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAAGGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGTCAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAAGG TGTCTCGGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGTTCT TCTCCCGGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCCT GTGCCTATGA CAGGATCGTG GTTGCAGGGG TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
 1561 AAGAAGCGCA AGGTTTGA

Figure 17(k)

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1587
 /note="1 to 1578 of FdDNase105correct"
 frag join(10..>729,<790..1587)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTG GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGCTGTCCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTT
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCGGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGGTTC
 1141 ACAGAGGTCA GGGAGTTTC CATTGTTCCC CTGCATGCGG CCCCCGGGGGA CGCAGTAGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACGCAGTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGC
 1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
T	Y	I	C	N.	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
E	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K
819	828	837	846	855	864												
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D
873	882	891	900	909	918												
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L
927	936	945	954	963	972												
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E
981	990	999	1008	1017	1026												
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D
1035	1044	1053	1062	1071	1080												
CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G
1089	1098	1107	1116	1125	1134												
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T
1143	1152	1161	1170	1179	1188												
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V
1197	1206	1215	1224	1233	1242												

GCC	GAG	ATC	GAT	T	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	GAG	AAA	TGG	GGC	
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G
1251				1260			1269			1278			1287			1296	
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R
1305				1314			1323			1332			1341			1350	
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L
1359				1368			1377			1386			1395			1404	
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R
1413				1422			1431			1440			1449			1458	
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
1467				1476			1485			1494			1503			1512	
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
1521				1530			1539			1548			1557			1566	
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG
S	D	H	Y	P	V	E	V	M	L	K	G	G	G	P	K	K	K
1575																	
CGC AAG GTT TGA 3'																	
R K V *																	

FIGURE 1

(A) pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS (pAS106)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 355 a 475 c 452 g 314 t
 ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGGGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCGGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCT TGCAATGCC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
 1321 CAGTGGTCAT CCATCCGCC GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

//

↳ NLS

Figure 18(B)

FOCUS FDDNASE106 1596 BP SS-DNA
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<799..1596)
 /note="1 to 1596 of PAS106.dna [Split]"
 frag 721..798
 /note="1 to 78 of 102/106linker"
 BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCCT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACCTC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCCTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCCTGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTC AGTGGCTGAT CCCCAGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TAAACTTCCA GGCTGCCTAT
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTGGA

Figure 18(c)

LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 RE YWCRDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1605 /note="1 to 1596 of FdDNase106correct"
 frag join(10..>729,<808..1605) /note="1 to 1596 of PAS106.dna [Split]"
 frag 730..807 /note="1 to 78 of 102/106linker"
 BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTC CCGAACCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAAATCA CACATGCTGT GTCGAGTGTG CACCGTGTCC AGCACCAGAG
 781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATGCCCTG
 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCACTGAGC CACTGGGACG GAACAGCTAT
 1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
 1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAAG GAGTTGCCA TTGTTCCCCT GCATGCGGCC
 1201 CGGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGGCACTTCA ATGCGGGCTG CAGCTATGTG
 1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
 1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
 1441 GCAGGGATGC TGCTCCGAGG GGCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
 1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
 1561 GTGATGCTGA AGGGGGCGG ACCAAAAAG AAGCGCAAGG TTTGA

File : PAS106.DNA
 Range : 1 - 1596 Mode : Normal
 Codon Table : Universal

FIGURE 18(D)

9	18	27	36	45	54
5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
---	---	---	---	---	---
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
---	---	---	---	---	---
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
---	---	---	---	---	---
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
---	---	---	---	---	---
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
---	---	---	---	---	---
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
---	---	---	---	---	---
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
---	---	---	---	---	---
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
---	---	---	---	---	---
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
---	---	---	---	---	---
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
---	---	---	---	---	---
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
---	---	---	---	---	---
G A L T S G V H T F P A V L Q S S G					

603 612 621 630 639 648
 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

 L Y S L S S V V T V P S S S L G T Q

657 666 675 684 693 702
 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K

711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG

 V E P K S C D K T H T C C V E C P P

765 774 783 792 801 810
 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG

 C P A P E G S G L K I A A F N I Q

819 828 837 846 855 864
 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG

 T F G E T K M S N A T L V S Y I V Q

873 882 891 900 909 918
 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG

 I L S R Y D I A L V Q E V R D S H L

927 936 945 954 963 972
 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT

 T A V G K L L D N L N Q D A P D T Y

981 990 999 1008 1017 1026
 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG

 H Y V V S E P L G R N S Y K E R Y L

1035 1044 1053 1062 1071 1080
 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT

 F V Y R P D Q V S A V D S Y Y Y D D

1089 1098 1107 1116 1125 1134
 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG

 G C E P C G N D T F N R E P A I V R

1143 1152 1161 1170 1179 1188
 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG

 F F S R F T E V R E F A I V P L H A

1197 1206 1215 1224 1233 1242

GCC CCG GGG GAC **S** A GTA GCC GAG ATC GAC GCT CTC TAT **S** GTC TAC CTG GAT
 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG
 Q L A Q A I S D H Y P V E V M L K G
 1575 1584 1593
 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3'
 G G P K K R K V *

FIGURE 19

(A) pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS (pAS107)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 354 a 474 c 448 g 314 t
 ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGGTCAA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAAGGTT CTTCTCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGCAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
 1561 GGCGGACCCA AAAAGAAGCG CAAGGTTGA

//

Ls NLS

Figure 19 (B)

J.OCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1590)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTGAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTTCCCGA CTGGGCTCTT CCCTTTAATC TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
 1561 GGCAGACCCA AAAAGAAGCG CAAGGTTTGA

Figure 1a (c)

LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<802..1599)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 730..801
 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGCTGTCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAAATCA CACATGCTGT GTGAGTGTG CACCGTGTCC AGCACCAGAG
 781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
 841 GCCACCCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
 901 GAGGTAGAG ACAGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
 1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTT
 1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTT GCCATTGTT CCCTGCATGC GGCCCCGGGG
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
 1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
 1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCGGAC TCGGCTCTTC CCTTTAACTT CCAGGGCTGCC
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
 1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

File : PAS107.DNA
 Range : 1 - 590 Mode : Normal
 Codon Table : Universal

FIGURE 19 (0)

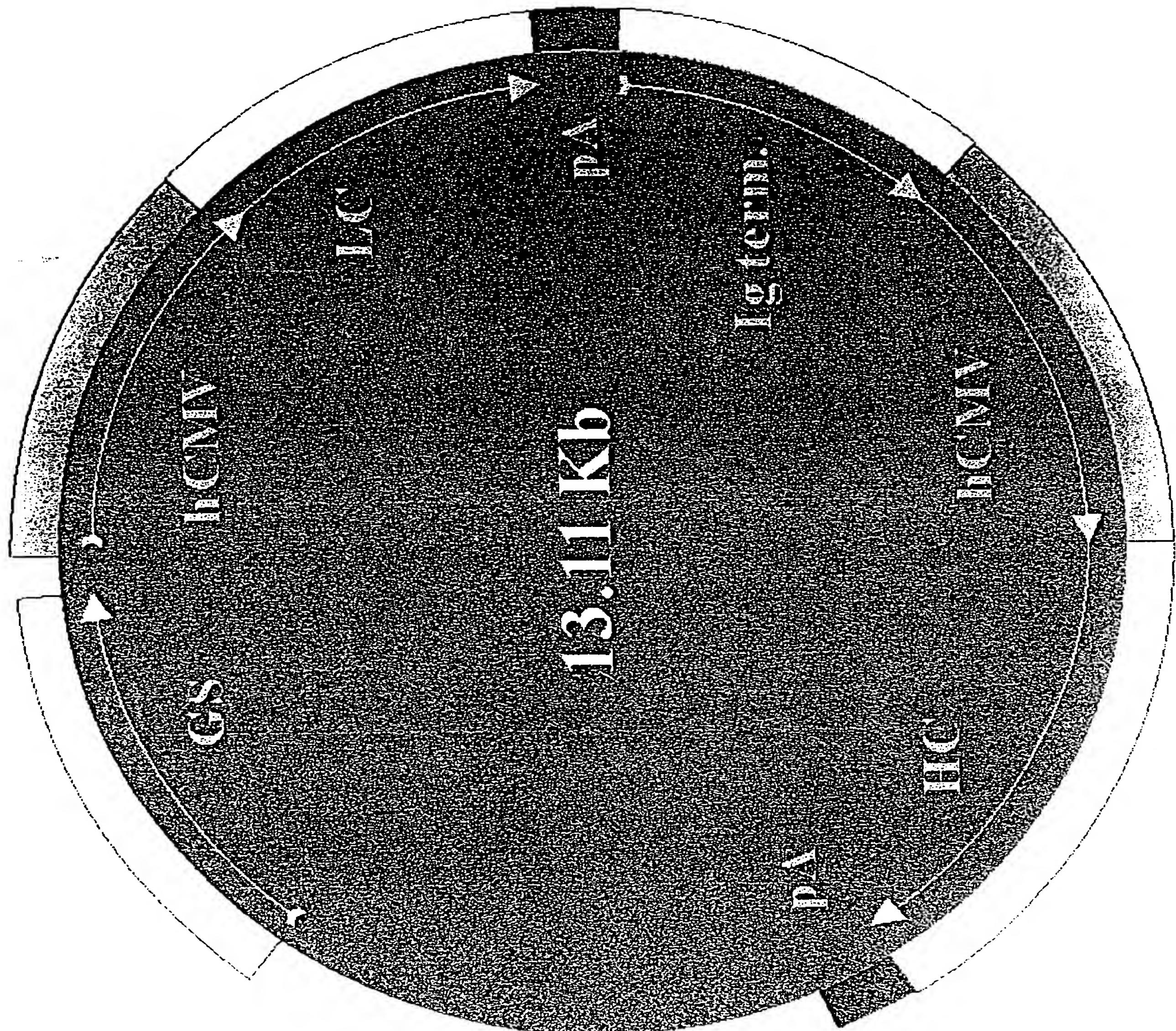
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M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
765	774	783	792	801	810												
TGC	CCA	GCA	CCT	GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
C	P	A	P	E	G	G	L	K	I	A	A	F	N	I	Q	T	F
819	828	837	846	855	864												
GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L
873	882	891	900	909	918												
AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A
927	936	945	954	963	972												
GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y
981	990	999	1008	1017	1026												
GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V
1035	1044	1053	1062	1071	1080												
TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C
1089	1098	1107	1116	1125	1134												
GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F
1143	1152	1161	1170	1179	1188												
TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A	A	P
1197	1206	1215	1224	1233	1242												

GGG GAC GCA GTA GAG ATC GAC GCT CTC TAT GAC GTC CTG GAT GTC CAA
 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557 1566
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA
 A Q A I S D H Y P V E V M L K G G G
 1575 1584
 CCC AAA AAG AAG CGC AAG GTT TGA 3'
 P K K K R K V *

Fig 20

Mammalian expression of humanised HMFG1-DNase constructs



8% SDS-PAGE reducing gel

Fig 21(A) Immuno-precipitation of metabolically labelled transient transfectants

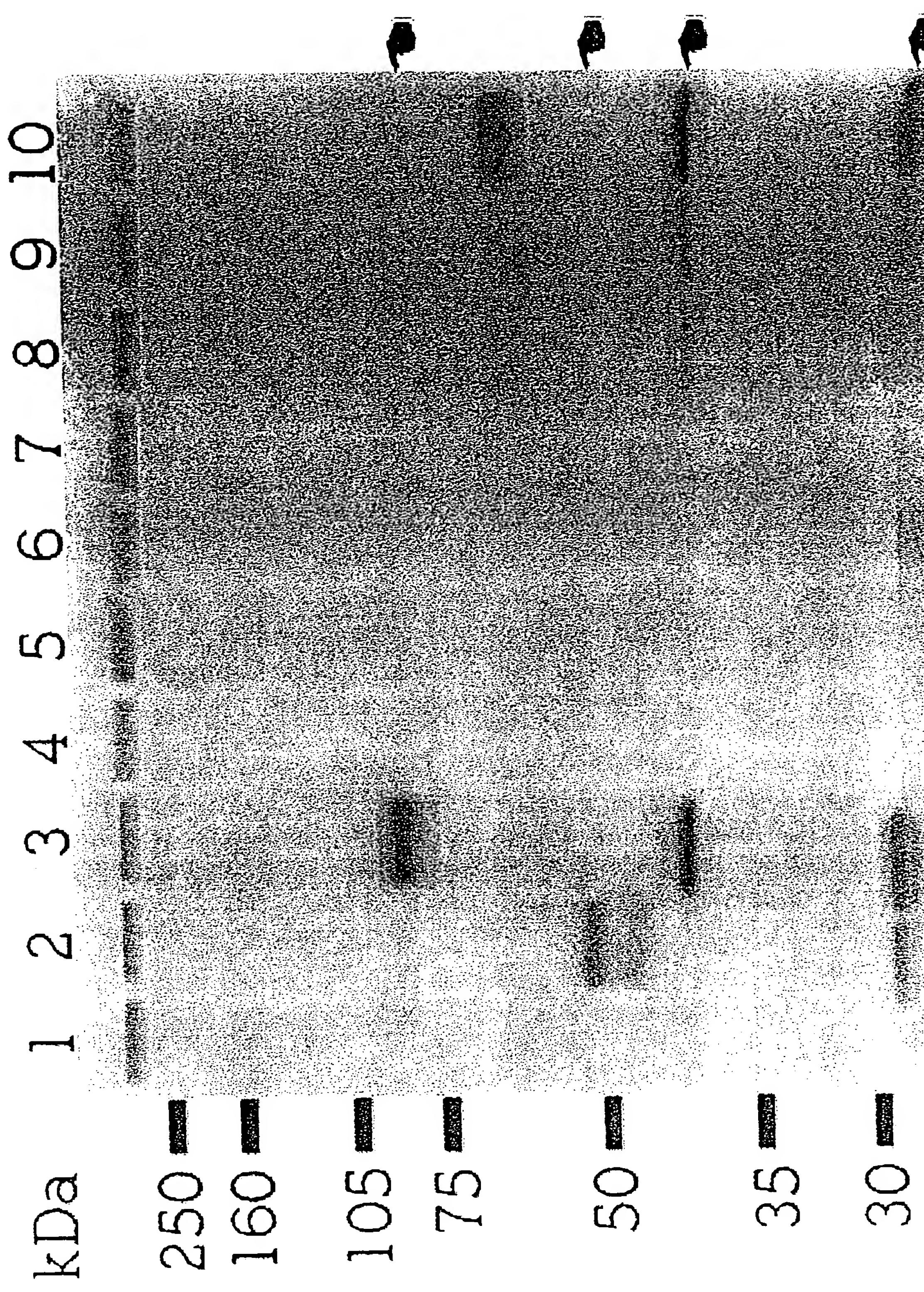


Fig 21 Immuno-precipitation of metabolically labelled transient transfectants

(B)

kDa 1 2 3 4 5 6 7 8 9 10

250

160

105

75

50

35

30

Fig 21 Immuno-precipitation of metabolically labelled transient transfectants

(c) 1 2 3 4 5 6 7 8 9 10 11

250 —
160 —
105 —
75 —
50 —
35 —
30 —
25 —
15 —

8% SDS-PAGE non-reducing gel

Fig 21 Immuno-precipitation of metabolically labelled transient transfectants

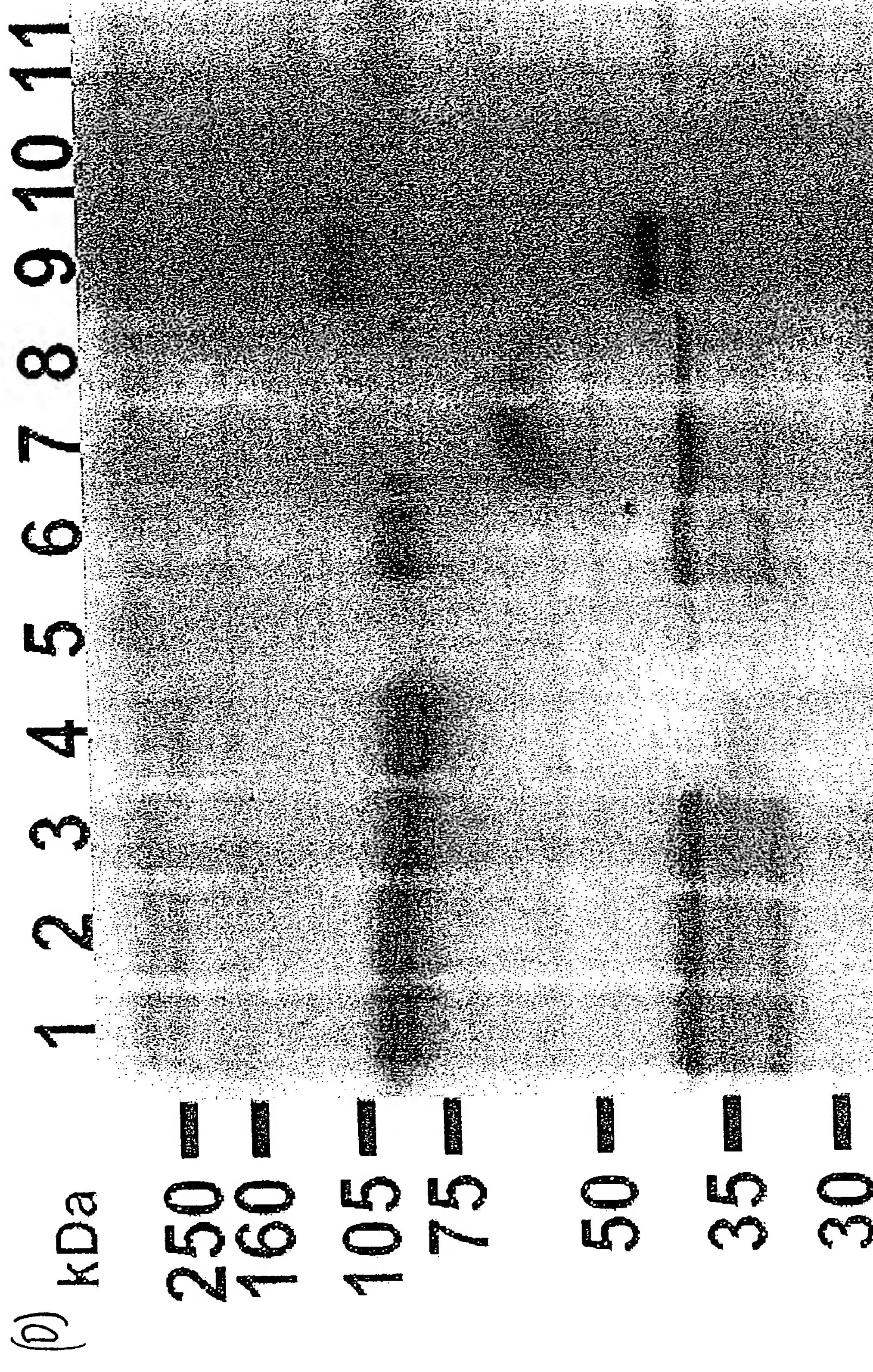


FIG 22

PDTTRP binding assay standard curve
(5' development)

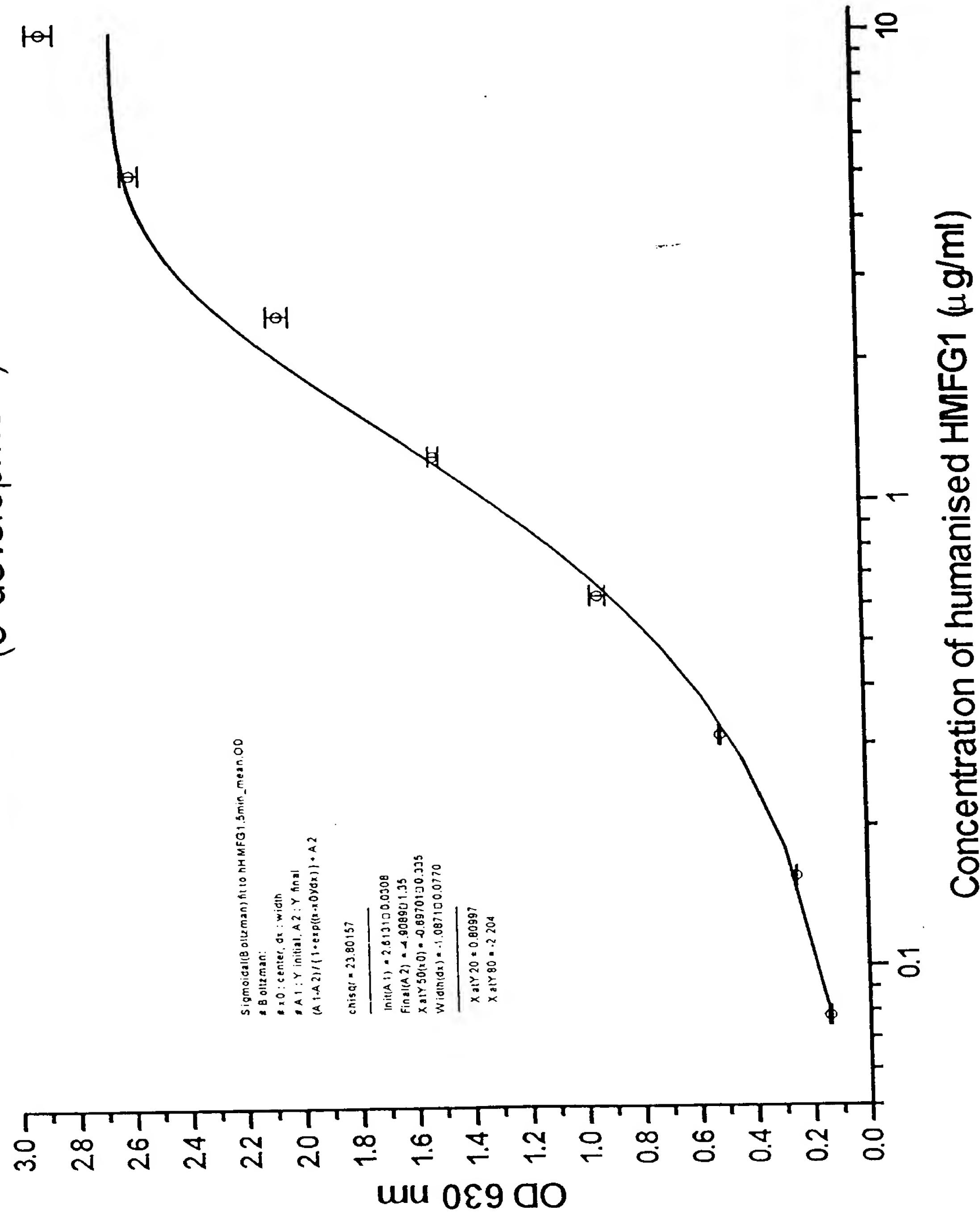


Fig 23

Corrected bovine DNase I standard curves
at various time points

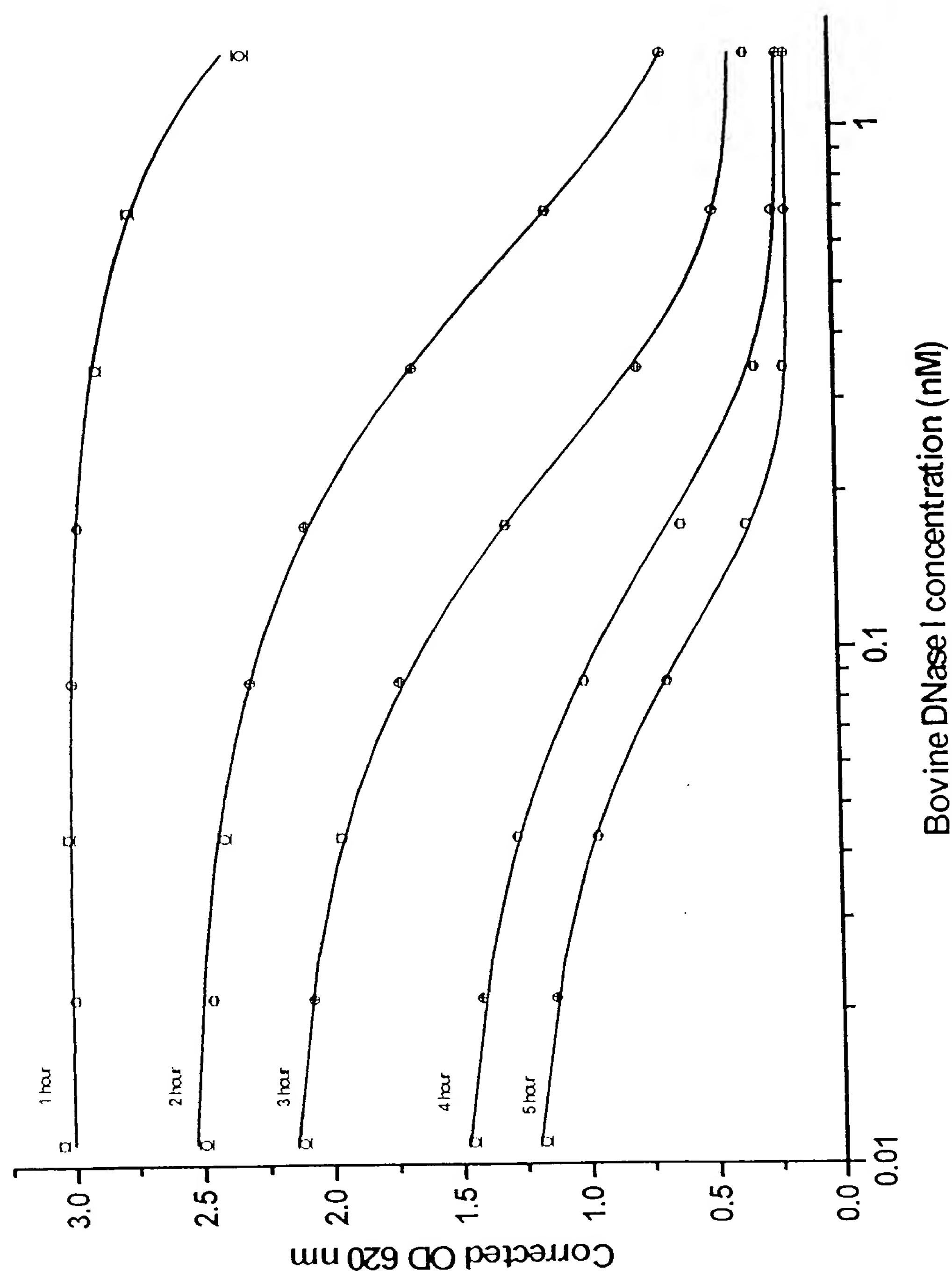


FIG 24

Corrected DNase I activity in transiently expressed
humanised human HMFG1-human DNase I constructs

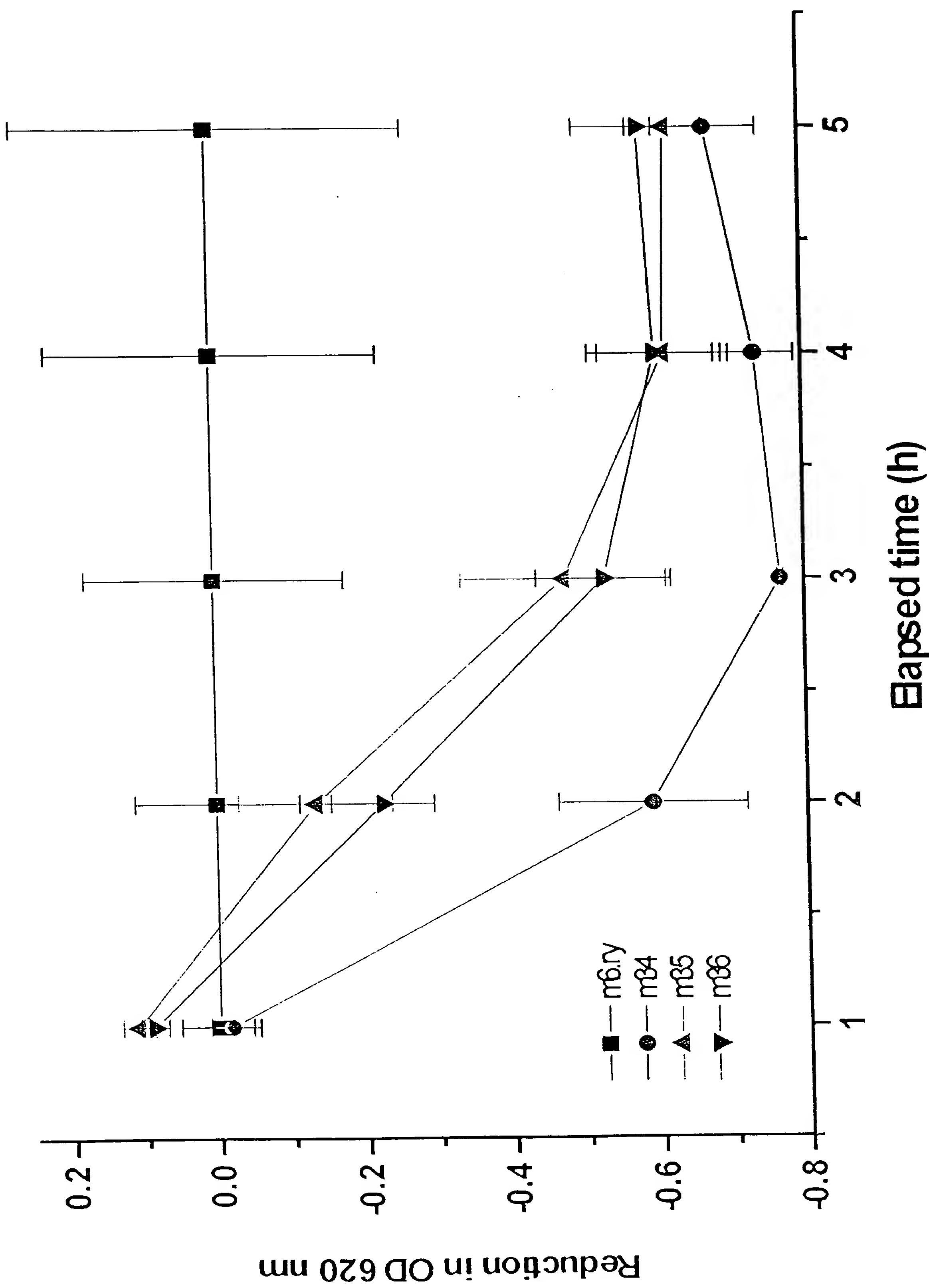


Fig 25

Corrected DNase I activity in transiently expressed
humanised HMG1 Rab'2-human DNase I fusions

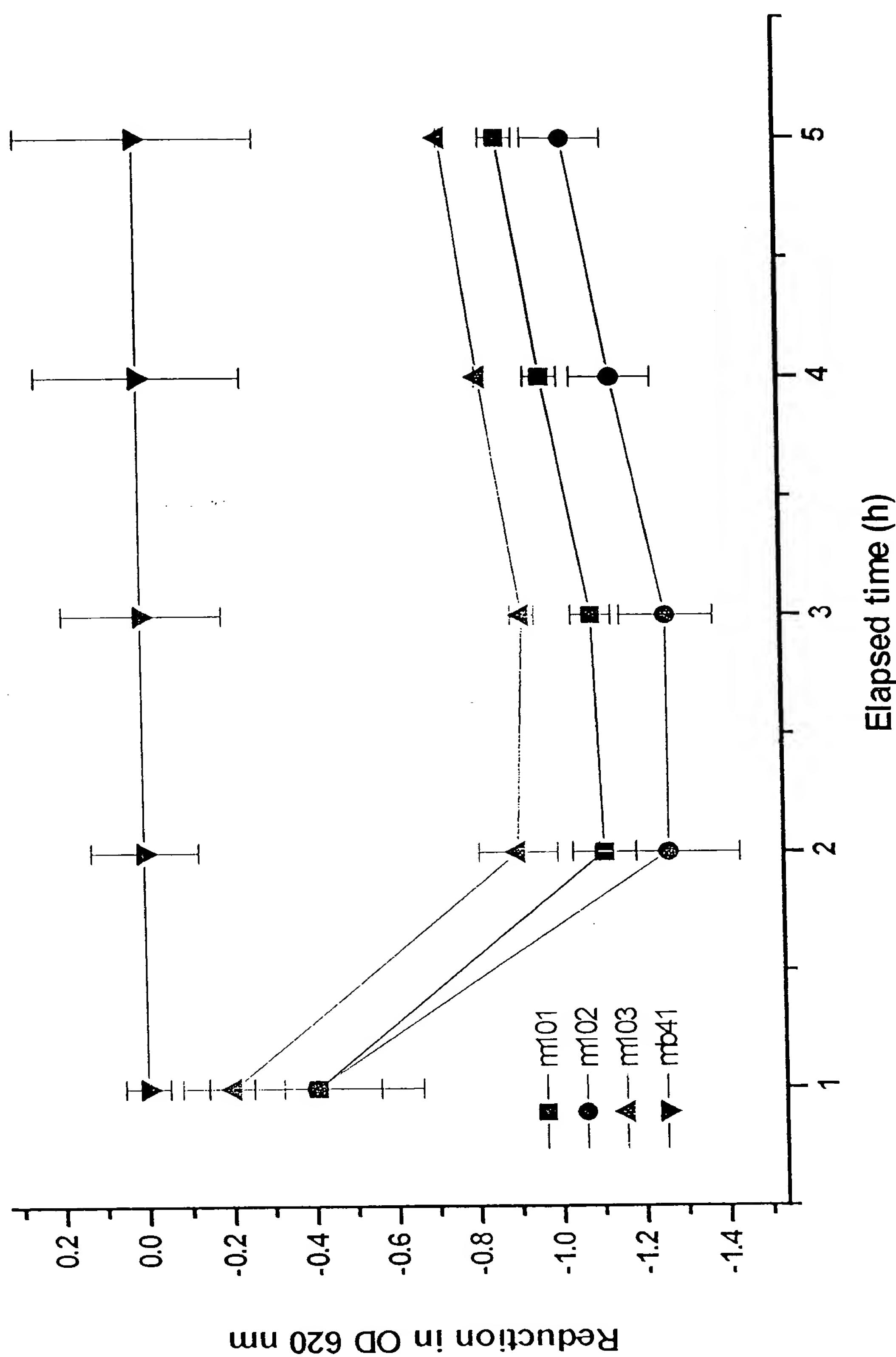


Fig. 26

Cytotoxicity Assay

10,000 cells/Well

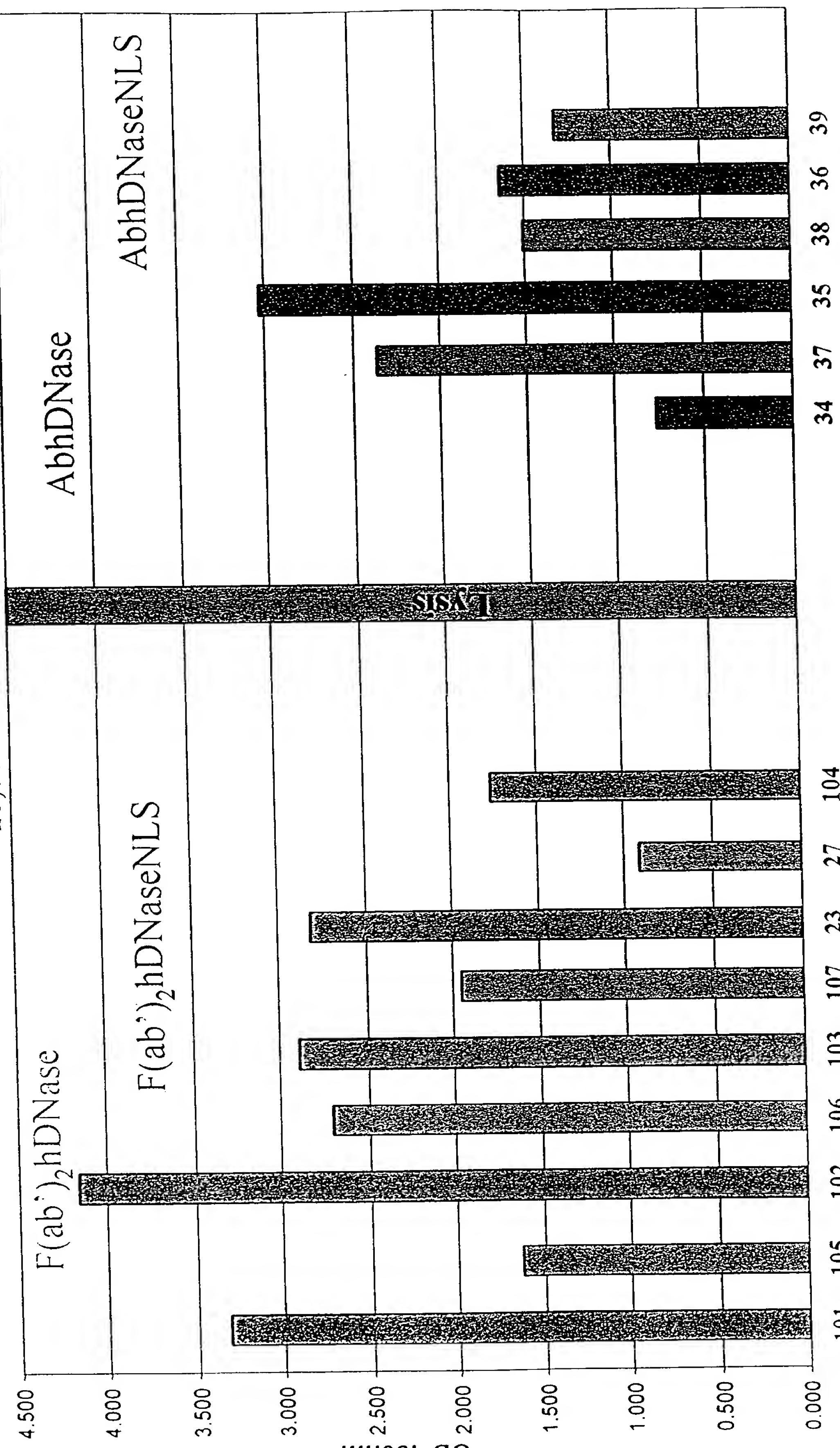
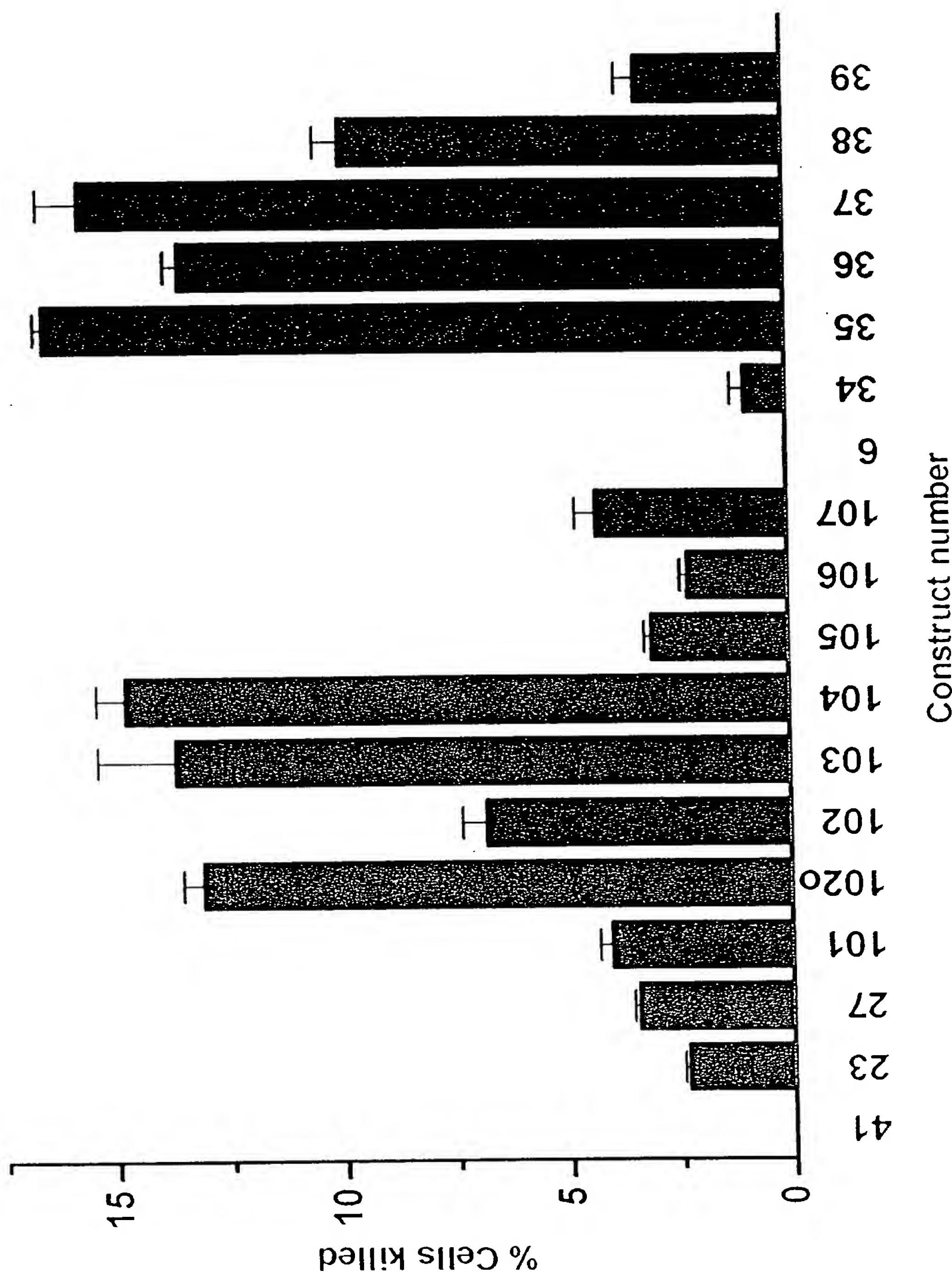


Fig 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample



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Figure 28

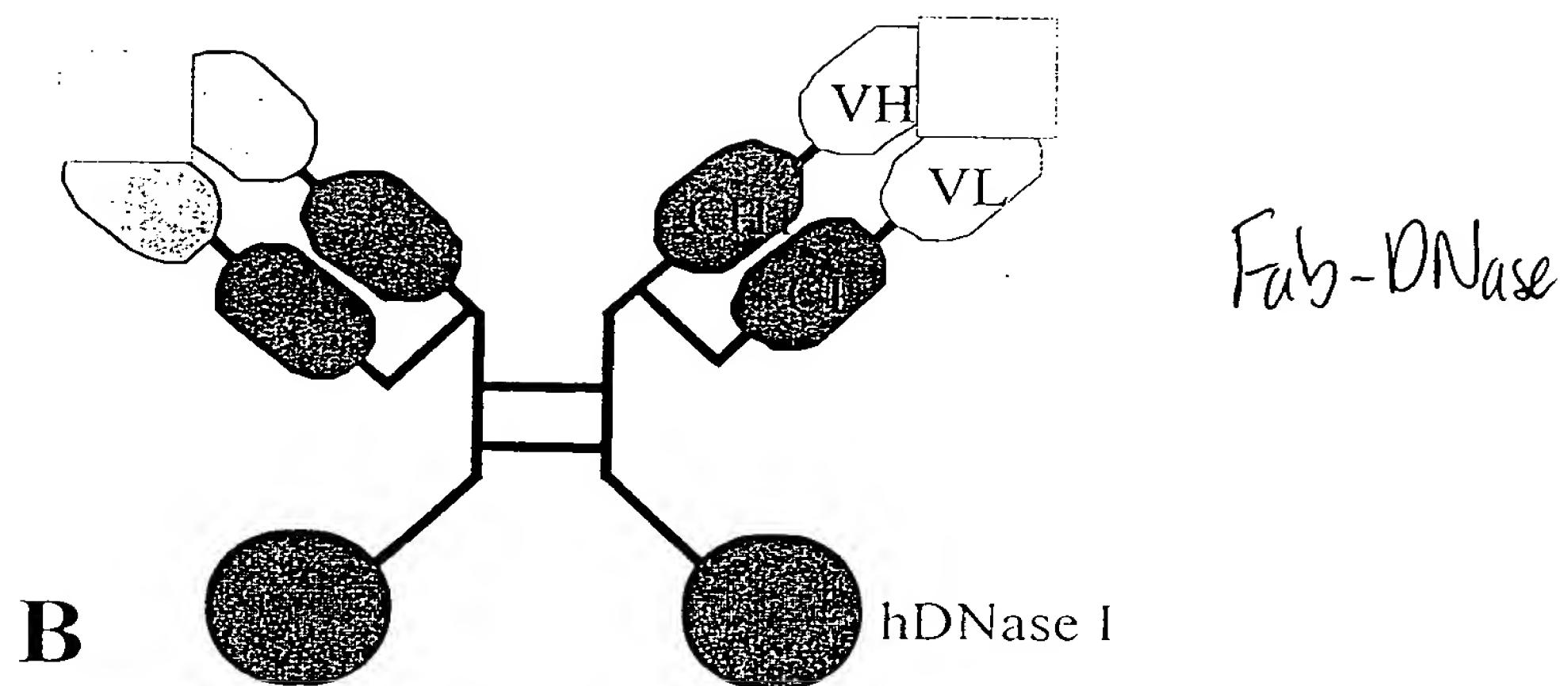
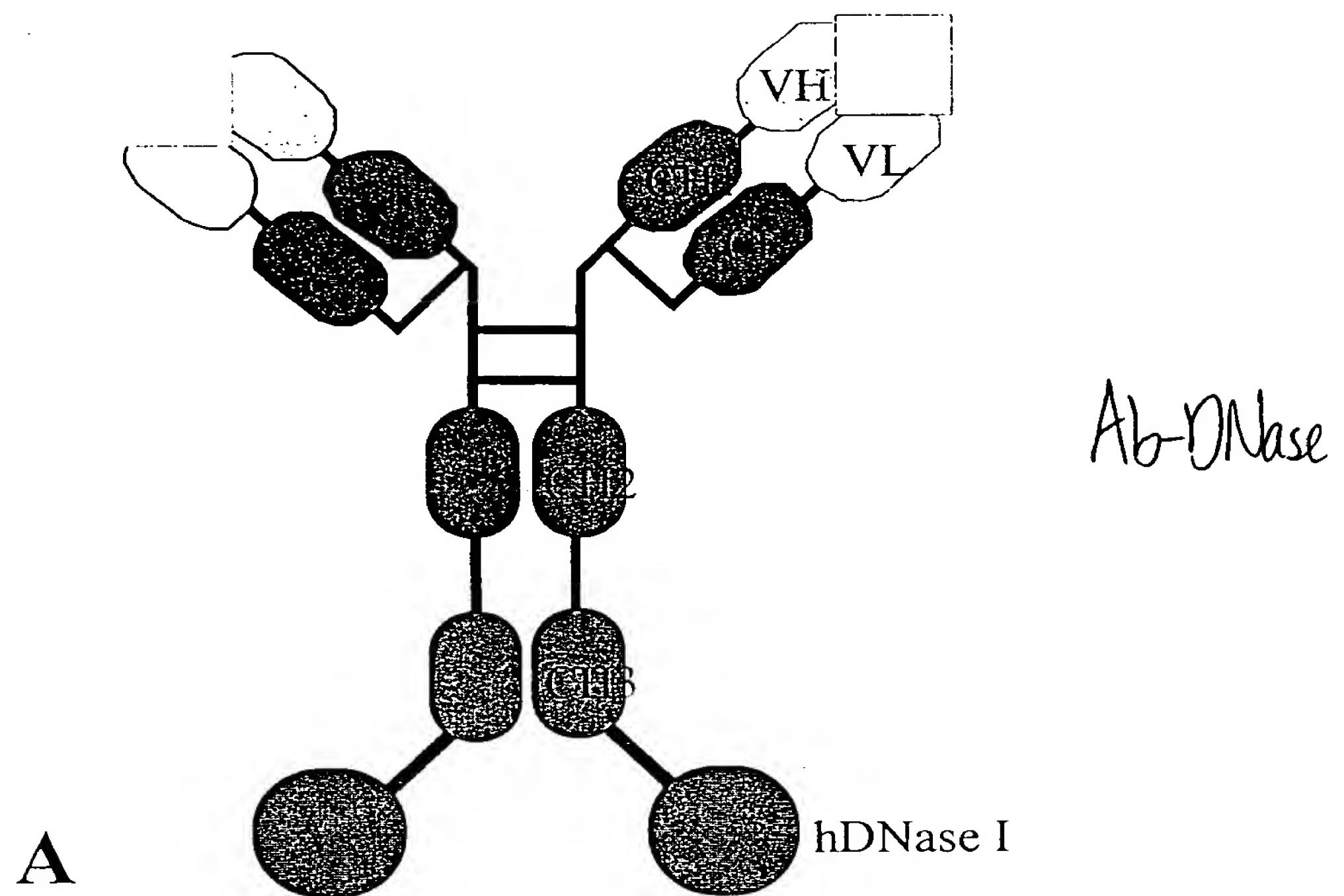
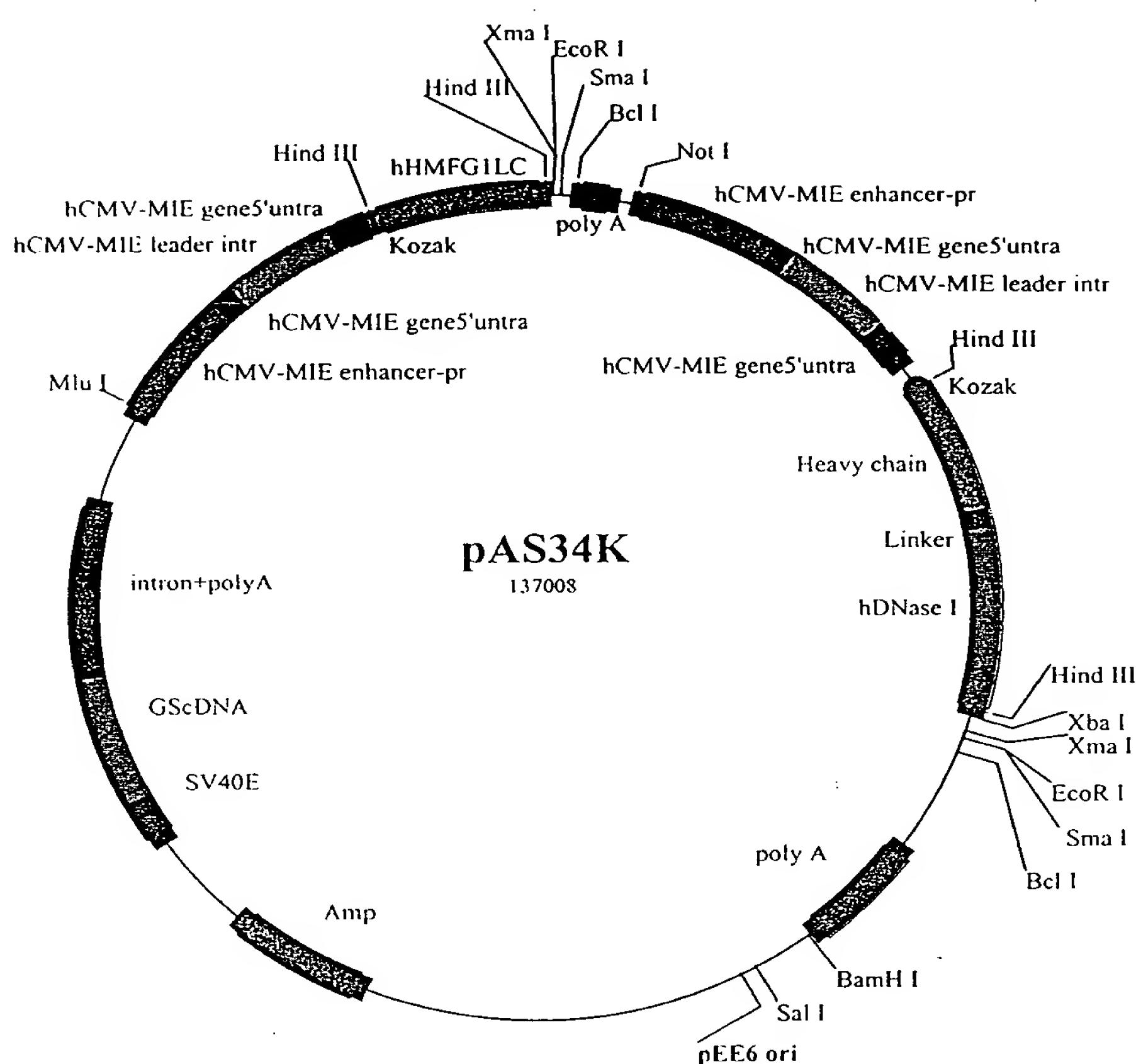


Figure 29



Ab-DNase

Figure 30

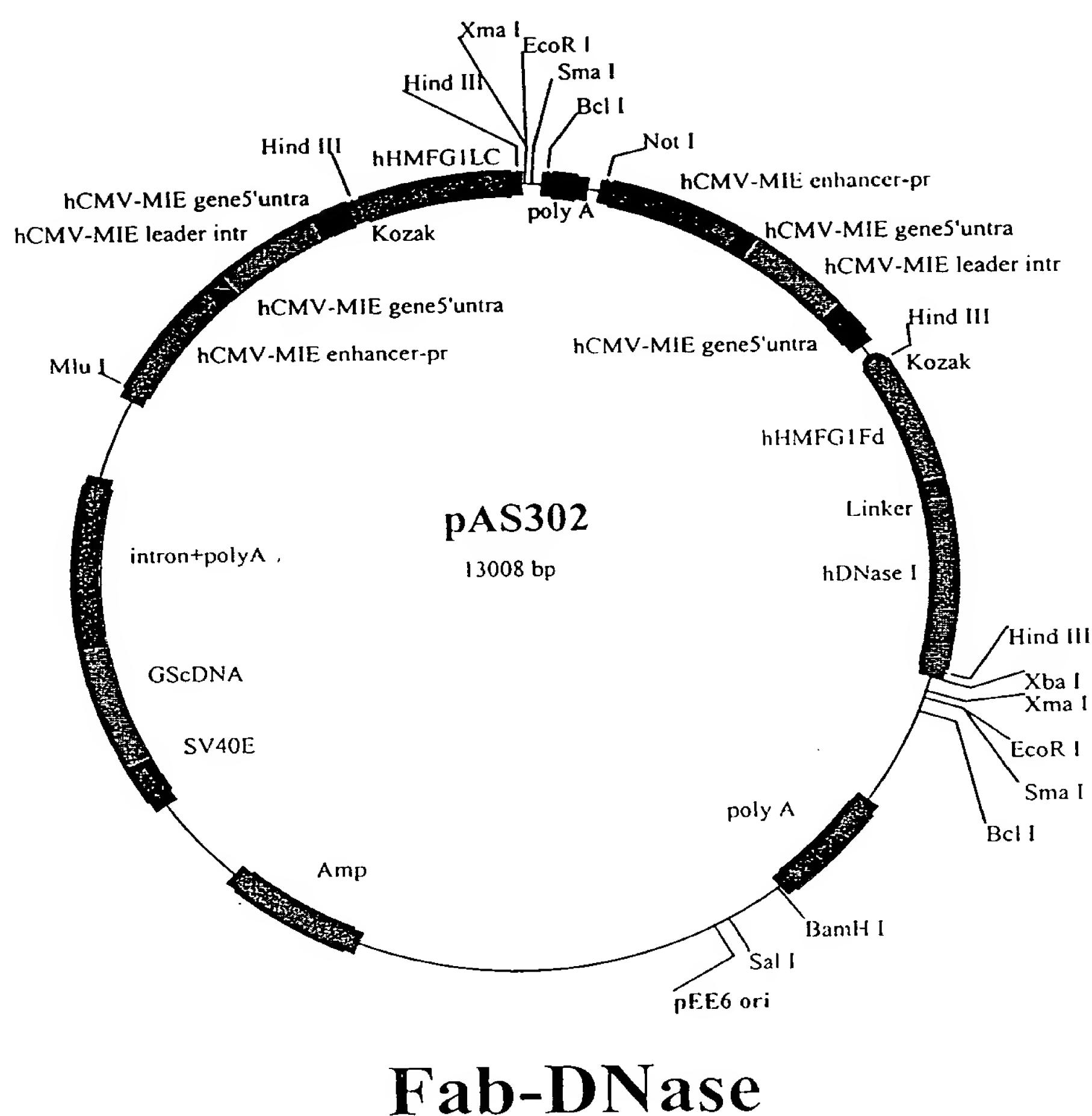
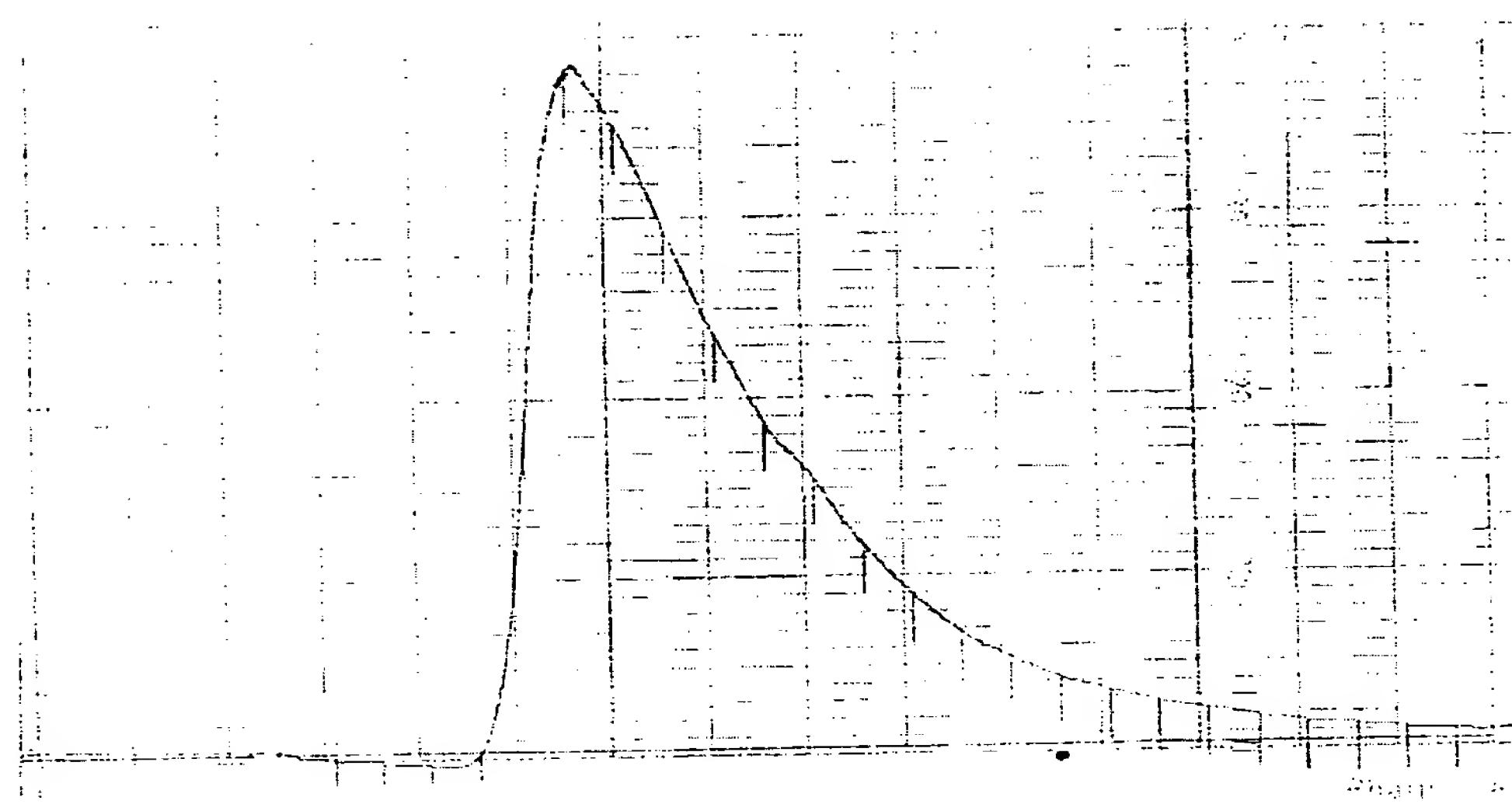
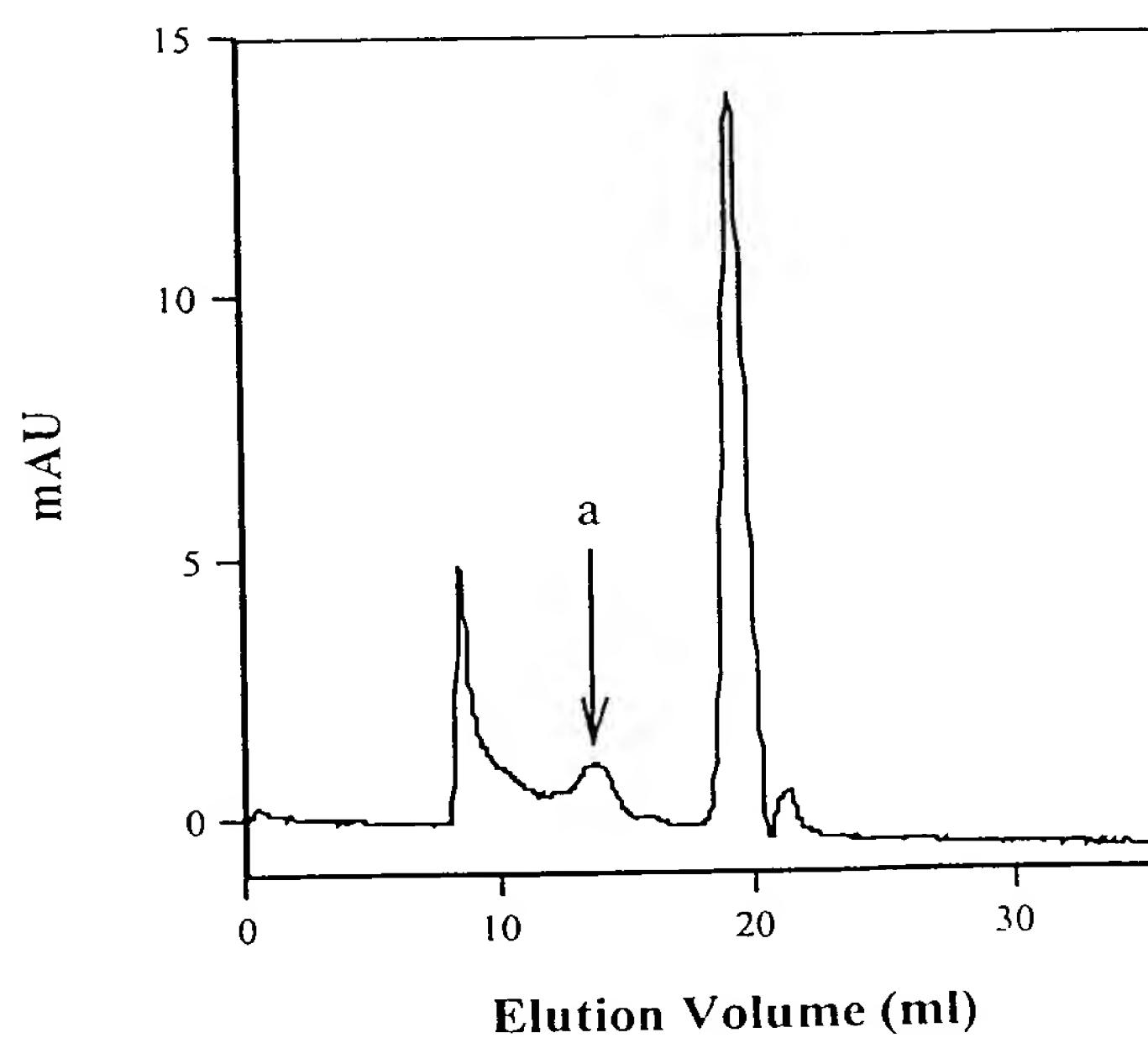


Figure 31

A

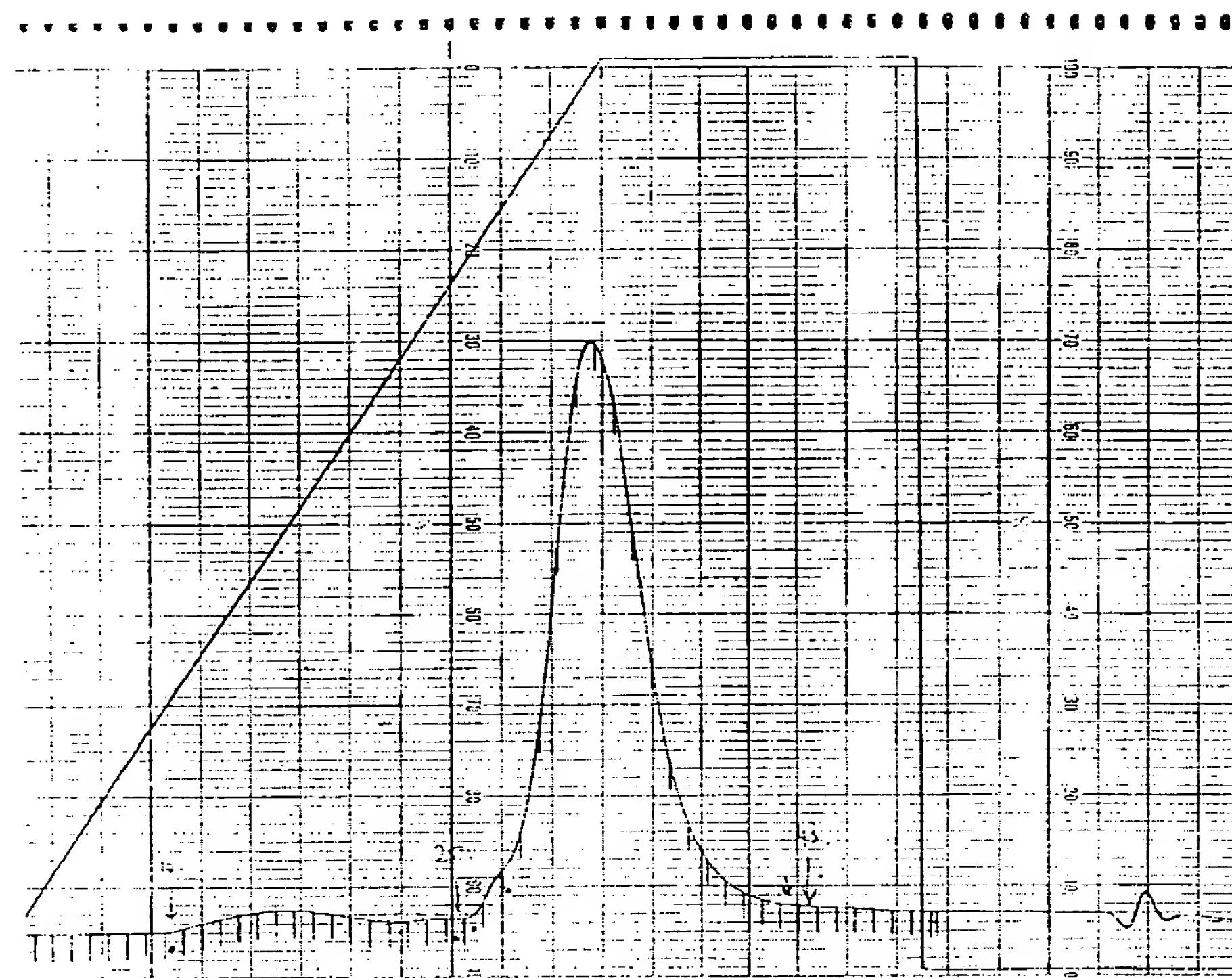


B

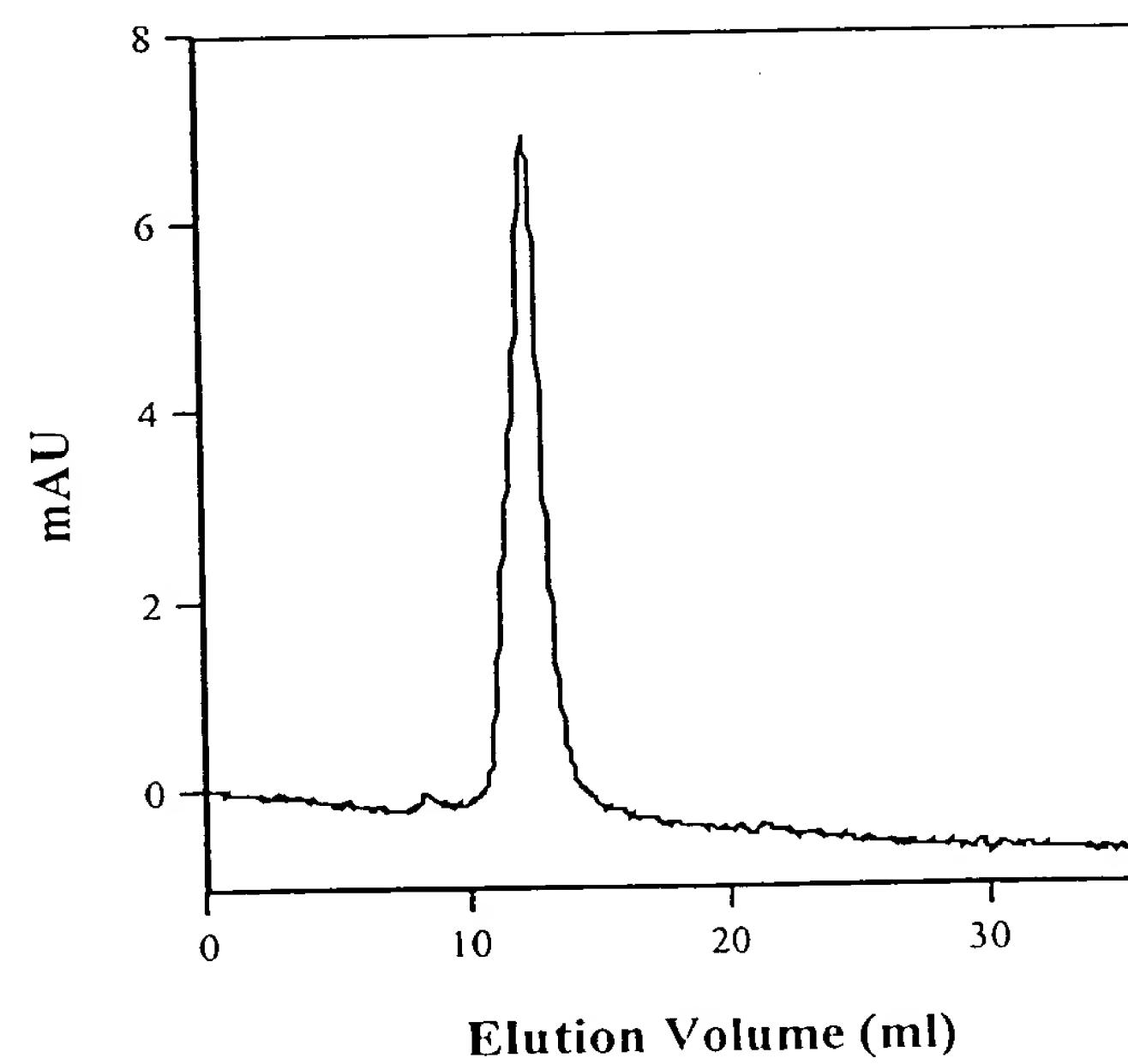


A

Figure 32



B



Elution Volume (ml)

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Figure 33

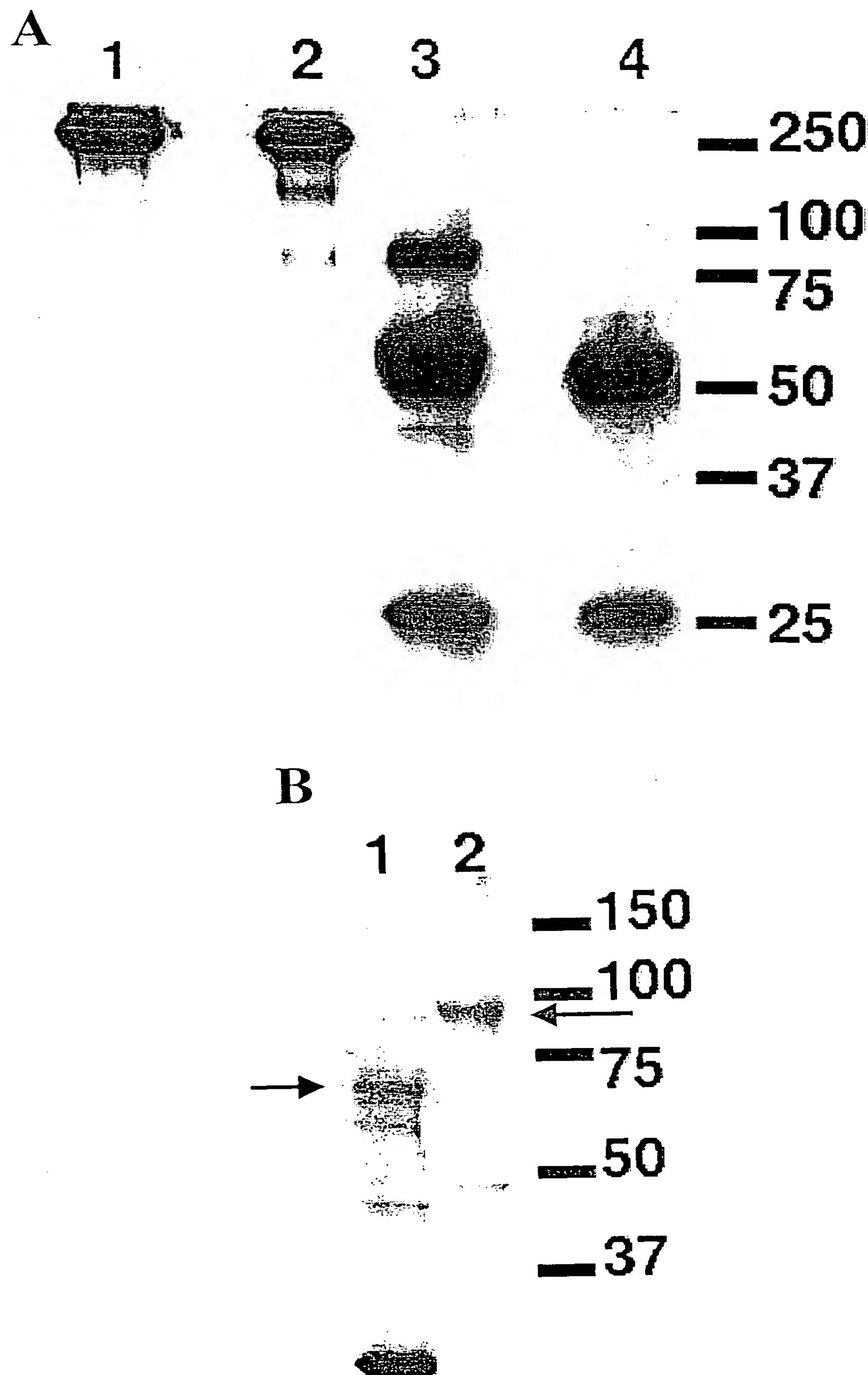
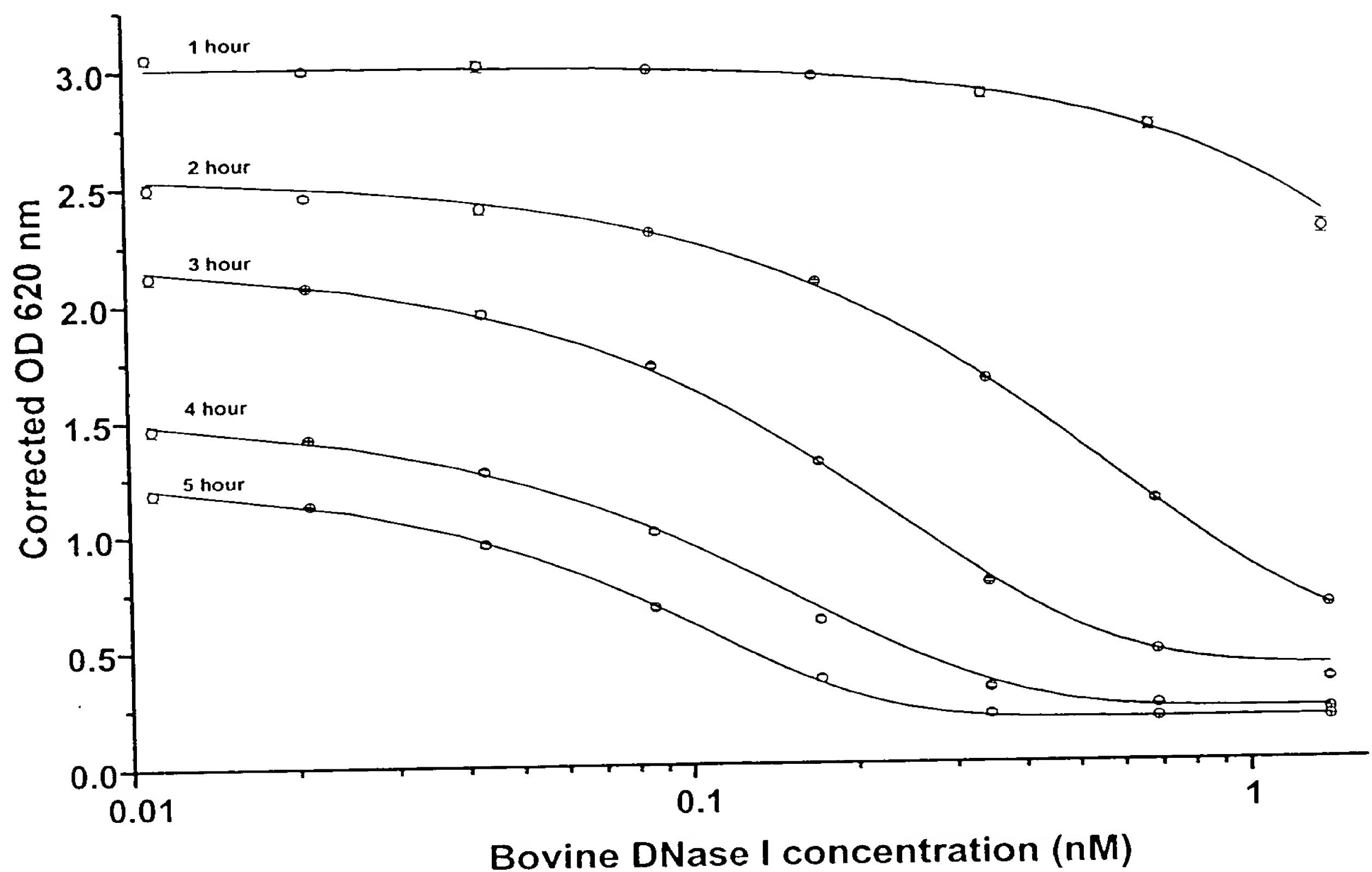


Figure 34

Bovine DNase I standard curves at various time points



A

Figure 34 – cont.

B

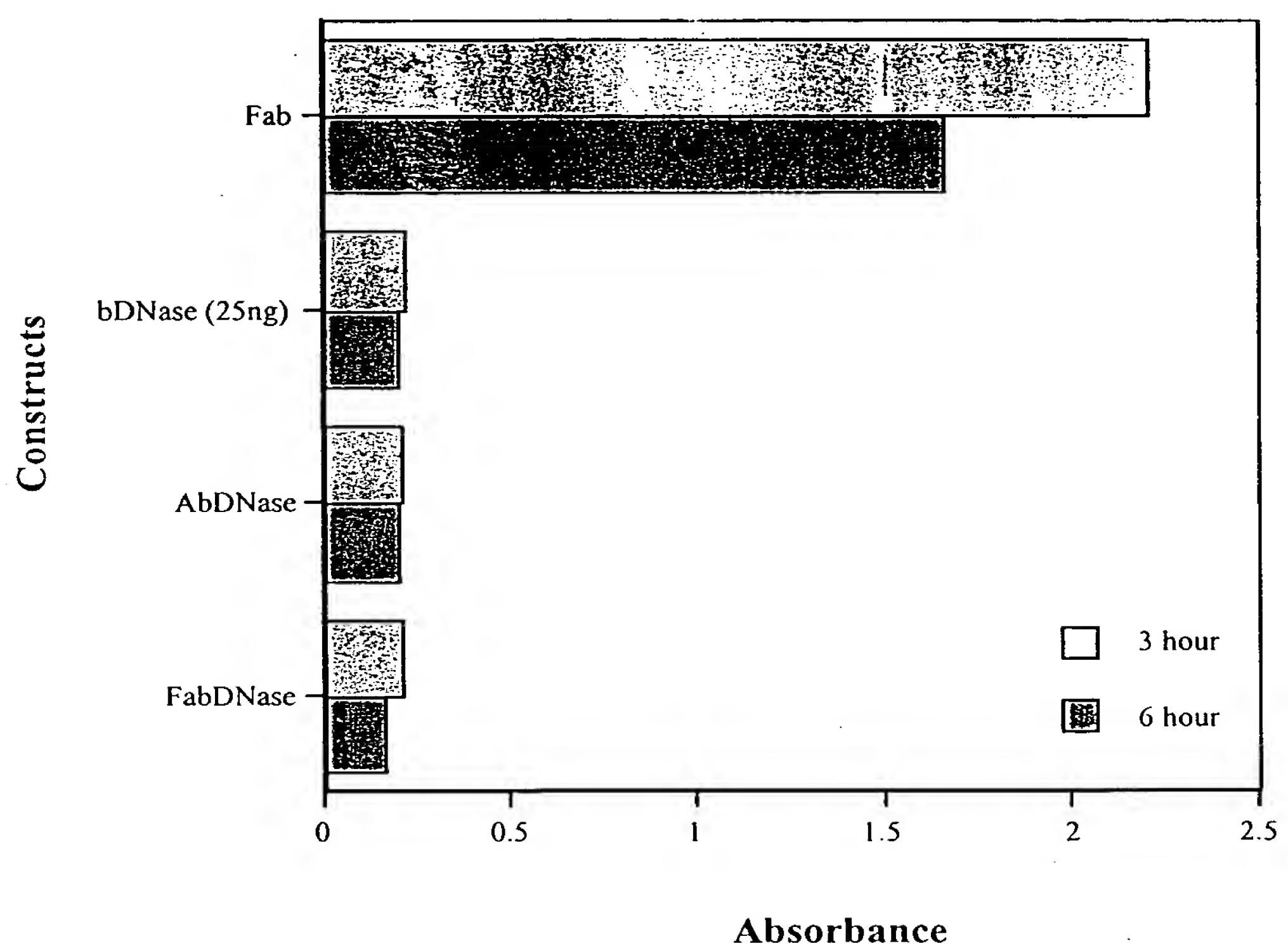


Figure 35

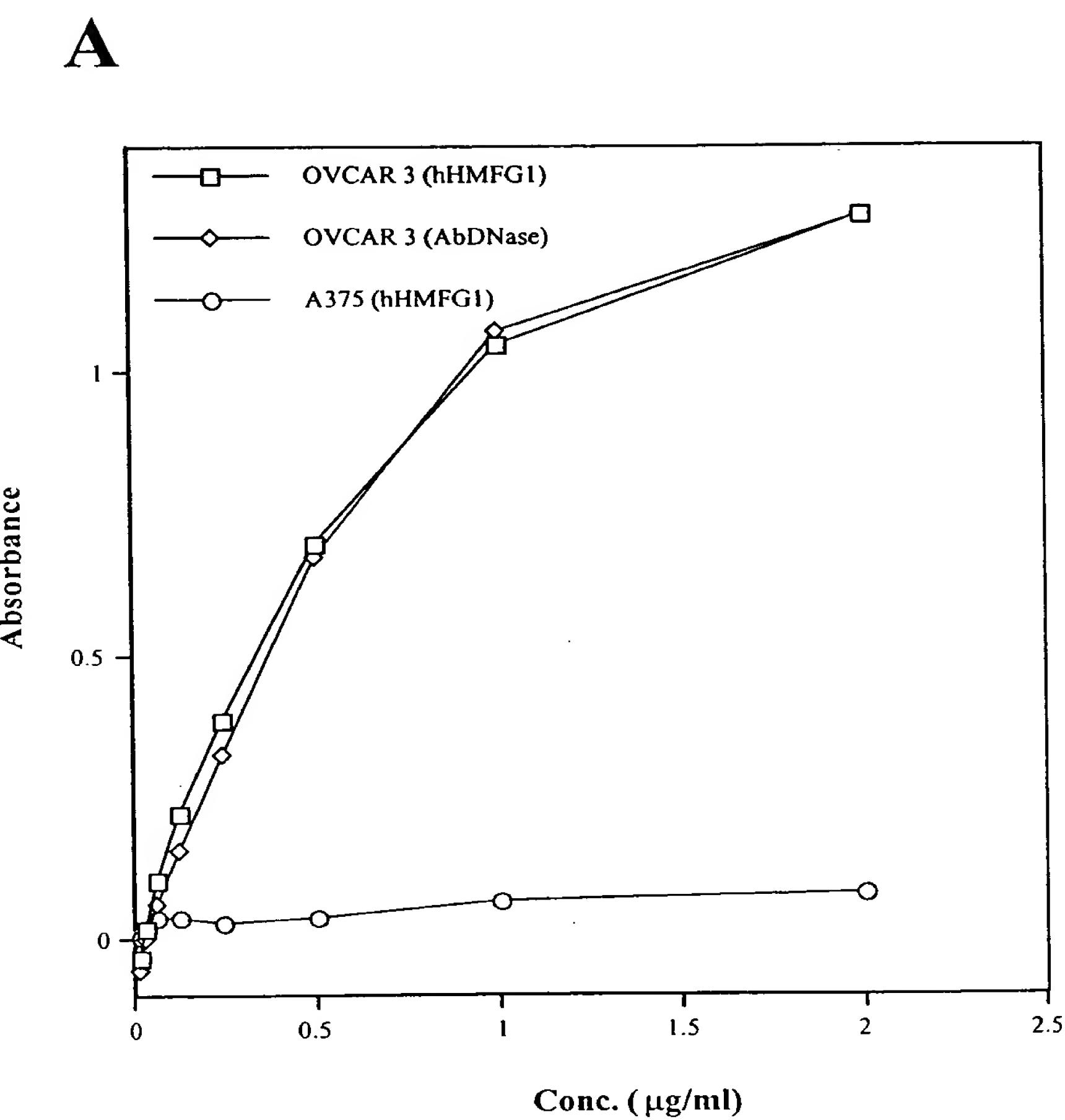
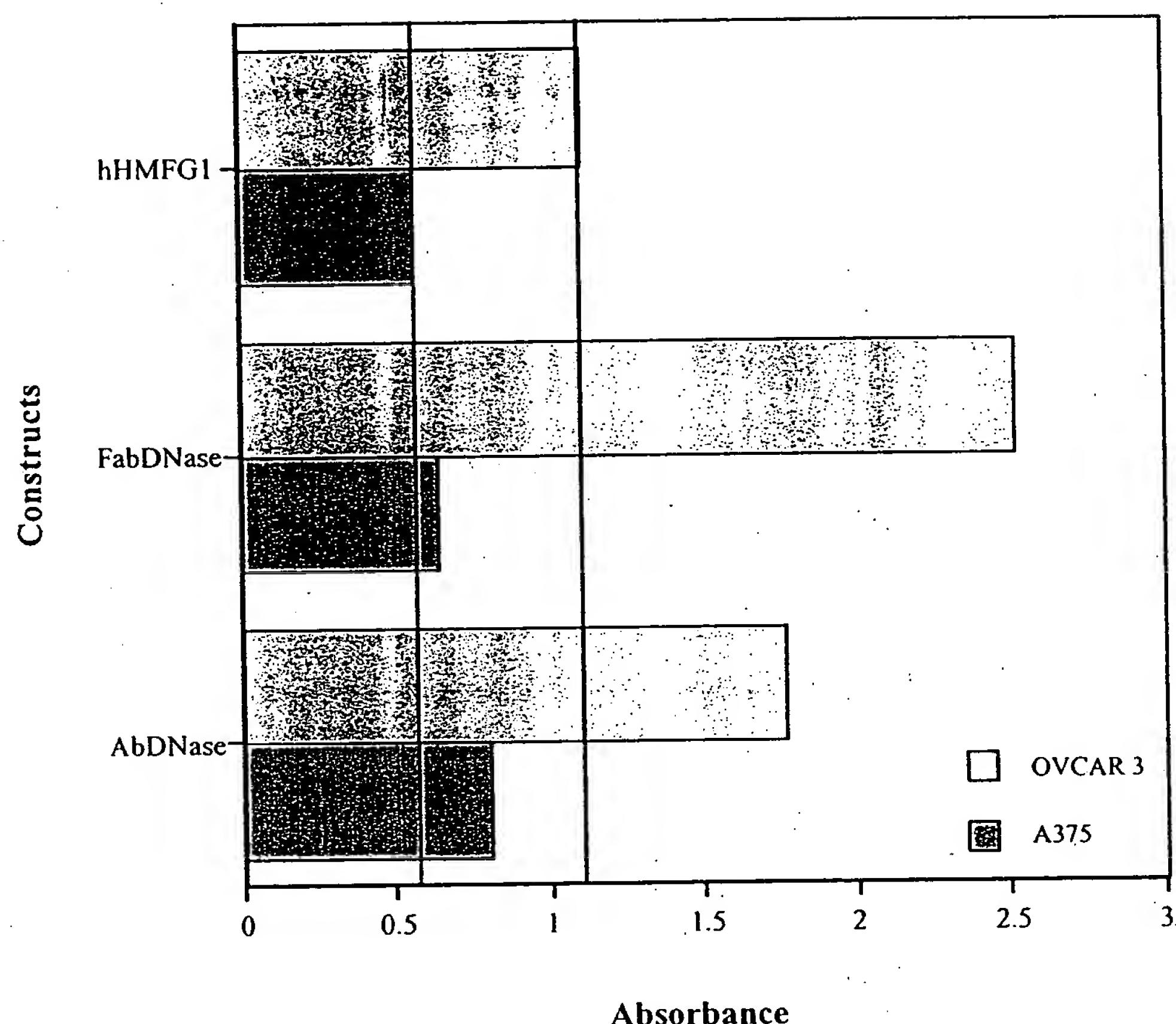


Figure 35 – cont.

B



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